

SEQUENCE LISTING

<110> Shimkets, Richard A.

<120> NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES

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<140> 09/991,053

<141> 2001-11-21

<150> USSN 60/123,667

<151> 1999-03-09

<150> 09/520,781

<151> 2000-03-08

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<170> PatentIn Ver. 2.1

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Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe Val			
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His Ile Pro Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr Leu			
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Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val Ala			
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Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
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Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
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Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
100 105 110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
115 120 125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
130 135 140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145 150 155 160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
165 170 175

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
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Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
195 200 205

Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
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Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Arg Glu Ile Ala
225 230 235 240

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
245 250 255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
260 265 270

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
275 280 285

Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
290 295 300

Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
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Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
325 330 335

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Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
355 360 365

Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
370 375 380

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
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Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
405 410 415

Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
420 425 430

Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
435 440 445

Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
450 455 460

Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
465 470 475 480

Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
485 490 495

Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
500 505 510

Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
515 520 525

Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
530 535 540

Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
545 550 555 560

Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
565 570 575

Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
580 585 590

Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
595 600 605

Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
610 615 620

His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
625 630 635 640

Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
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Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
660 665 670

Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
675 680 685

Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
690 695 700

Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
705 710 715 720

Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
725 730 735

Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
740 745 750

Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
755 760 765

Glu Pro Ser Arg Gly Thr Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
770 775 780

Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
785 790 795 800

Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
805 810 815

Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
820 825 830

Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
835 840 845

Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
850 855 860

Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
865 870 875 880

Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
885 890 895

Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
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His Leu Thr Thr Tyr Ser His Gln Lys Gln His
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cgctgtacca gttcgctccg agcccccggcc gcctgtccgt cgatgcacccg aaaagggtga 180
agtagagaaa taaagtctcc ccgctgaact act atg agg tca gaa gcc ttg ctg 234
Met Arg Ser Glu Ala Leu Leu
1 5

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Leu Tyr Phe Thr Leu Leu His Phe Ala Gly Ala Gly Phe Pro Glu Asp
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Ser Glu Pro Ile Ser Ile His Gly Asn Tyr Thr Lys Gln Tyr Pro
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gtg ttt gtg ggc cac aag cca gga cgg aac acc aca cag agg cac agg 378
Val Phe Val Gly His Lys Pro Gly Arg Asn Thr Thr Gln Arg His Arg
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ctg gac atc cag atg att atg atc atg aac gga acc ctc tac att gct 426
Leu Asp Ile Gln Met Ile Met Asn Gly Thr Leu Tyr Ile Ala
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gct agg gac cat att tat act gtt gat ata gac aca tca cac acg gaa 474
Ala Arg Asp His Ile Tyr Thr Val Asp Ile Asp Thr Ser His Thr Glu
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gaa att tat tgt agc aaa aaa ctg aca tgg aaa tct aga cag gcc gat 522
Glu Ile Tyr Cys Ser Lys Lys Leu Thr Trp Lys Ser Arg Gln Ala Asp
90 95 100

gta gac aca tgc aga atg aag gga aaa cat aag gat gag tgc cac aac 570
Val Asp Thr Cys Arg Met Lys Gly Lys His Lys Asp Glu Cys His Asn
105 110 115

ttt att aaa gtt ctt cta aag aaa aac gat gat gca ttg ttt gtc tgt 618
Phe Ile Lys Val Leu Leu Lys Lys Asn Asp Ala Leu Phe Val Cys
120 125 130 135

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Gly Thr Asn Ala Phe Asn Pro Ser Cys Arg Asn Tyr Lys Met Asp Thr
140 145 150

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Leu Glu Pro Phe Gly Asp Glu Phe Ser Gly Met Ala Arg Cys Pro Tyr			
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gat gcc aaa cat gcc aac gtt gca ctg ttt gca gat gga aaa cta tac		762	
Asp Ala Lys His Ala Asn Val Ala Leu Phe Ala Asp Gly Lys Leu Tyr			
170	175	180	
tca gcc aca gtg act gac ttc ctt gcc att gac gca gtc att tac cgg		810	
Ser Ala Thr Val Thr Asp Phe Leu Ala Ile Asp Ala Val Ile Tyr Arg			
185	190	195	
agt ctt gga gaa agc cct acc ctg cgg acc gtc aag cac gat tca aaa		858	
Ser Leu Gly Ser Pro Thr Leu Arg Thr Val Lys His Asp Ser Lys			
200	205	210	215
tgg ttg aaa gaa cca tac ttt gtt caa gcc gtg gat tac gga gat tat		906	
Trp Leu Lys Glu Pro Tyr Phe Val Gln Ala Val Asp Tyr Gly Asp Tyr			
220	225	230	
atc tac ttc ttc ttc agg gaa ata gca gtg gag tat aac acc atg gga		954	
Ile Tyr Phe Phe Arg Glu Ile Ala Val Glu Tyr Asn Thr Met Gly			
235	240	245	
aag gta gtt ttc cca aga gtg gct cag gtt tgt aag aat gat atg gga		1002	
Lys Val Val Phe Pro Arg Val Ala Gln Val Cys Lys Asn Asp Met Gly			
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gga tct caa aga gtc ctg gag aaa cag tgg acg tcg ttc ctg aag gcg		1050	
Gly Ser Gln Arg Val Leu Glu Lys Gln Trp Thr Ser Phe Leu Lys Ala			
265	270	275	
cgc ttg aac tgc tca gtt cct gga gac tct cat ttt tat ttc aac att		1098	
Arg Leu Asn Cys Ser Val Pro Gly Asp Ser His Phe Tyr Phe Asn Ile			
280	285	290	295
ctc cag gca gtt aca gat gtg att cgt atc aac ggg cgt gat gtt gtc		1146	
Leu Gln Ala Val Thr Asp Val Ile Arg Ile Asn Gly Arg Asp Val Val			
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ctg gca acg ttt tct aca cct tat aac agc atc cct ggg tct gca gtc		1194	
Leu Ala Thr Phe Ser Thr Pro Tyr Asn Ser Ile Pro Gly Ser Ala Val			
315	320	325	
tgt gcc tat gac atg ctt gac att gcc agt gtt ttt act ggg aga ttc		1242	
Cys Ala Tyr Asp Met Leu Asp Ile Ala Ser Val Phe Thr Gly Arg Phe			
330	335	340	
aag gaa cag aag tct cct gat tcc acc tgg aca cca gtt cct gat gaa		1290	
Lys Glu Gln Lys Ser Pro Asp Ser Thr Trp Thr Pro Val Pro Asp Glu			
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cga gtt cct aag ccc agg cca ggt tgc tgt gct ggc tca tcc tcc tta		1338	
Arg Val Pro Lys Pro Arg Pro Gly Cys Cys Ala Gly Ser Ser Ser Leu			
360	365	370	375
gaa aga tat gca acc tcc aat gag ttc cct gat gat acc ctg aac ttc		1386	

Glu Arg Tyr Ala Thr Ser Asn Glu Phe Pro Asp Asp Thr Leu Asn Phe			
380	385	390	
atc aag acg cac ccg ctc atg gat gag gca gtg ccc tcc atc ttc aac	1434		
Ile Lys Thr His Pro Leu Met Asp Glu Ala Val Pro Ser Ile Phe Asn			
395	400	405	
agg cca tgg ttc ctg aga aca atg gtc aga tac cgc ctt acc aaa att	1482		
Arg Pro Trp Phe Leu Arg Thr Met Val Arg Tyr Arg Leu Thr Lys Ile			
410	415	420	
gca gtg gac aca gct gct ggg cca tat cag aat cac act gtg gtt ttt	1530		
Ala Val Asp Thr Ala Ala Gly Pro Tyr Gln Asn His Thr Val Val Phe			
425	430	435	
ctg gga tca gag aag gga atc atc ttg aag ttt ttg gcc aga ata gga	1578		
Leu Gly Ser Glu Lys Gly Ile Ile Leu Lys Phe Leu Ala Arg Ile Gly			
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aat agt ggt ttt cta aat gac agc ctt ttc ctg gag gag atg agt gtt	1626		
Asn Ser Gly Phe Leu Asn Asp Ser Leu Phe Leu Glu Glu Met Ser Val			
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tac aac tct gaa aaa tgc agc tat gat gga gtc gaa gac aaa agg atc	1674		
Tyr Asn Ser Glu Lys Cys Ser Tyr Asp Gly Val Glu Asp Lys Arg Ile			
475	480	485	
atg ggc atg cag ctg gac aga gca agc agc tct ctg tat gtt gcg ttc	1722		
Met Gly Met Gln Leu Asp Arg Ala Ser Ser Ser Leu Tyr Val Ala Phe			
490	495	500	
tct acc tgt gtg ata aag gtt ccc ctt ggc cgg tgt gaa cga cat ggg	1770		
Ser Thr Cys Val Ile Lys Val Pro Leu Gly Arg Cys Glu Arg His Gly			
505	510	515	
aag tgt aaa aaa acc tgt att gcc tcc aga gac cca tat tgt gga tgg	1818		
Lys Cys Lys Lys Thr Cys Ile Ala Ser Arg Asp Pro Tyr Cys Gly Trp			
520	525	530	535
ata aag gaa ggt ggt gcc tgc agc cat tta tca ccc aac agc aga ctg	1866		
Ile Lys Glu Gly Gly Ala Cys Ser His Leu Ser Pro Asn Ser Arg Leu			
540	545	550	
act ttt gag cag gac ata gag cgt ggc aat aca gat ggt ctg ggg gac	1914		
Thr Phe Glu Gln Asp Ile Glu Arg Gly Asn Thr Asp Gly Leu Gly Asp			
555	560	565	
tgt cac aat tcc ttt gtg gca ctg aat gga gtg att cgg gaa agt tac	1962		
Cys His Asn Ser Phe Val Ala Leu Asn Gly Val Ile Arg Glu Ser Tyr			
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ctc aaa ggc cac gac cag ctg gtt ccc gtc acc ctc ttg gcc att gca	2010		
Leu Lys Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala			
585	590	595	
gtc atc ctg gct ttc gtc atg ggg gcc gtc ttc tcg ggc atc acc gtc	2058		
Val Ile Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val			

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Tyr	Cys	Val	Cys	Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg
				620
				625
				630
aag gag aag gag ctc acc cac tc ^g cg ^c cg ^g ggc tcc at ^g agc agc gtc				2154
Lys	Glu	Lys	Glu	Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val
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				645
acc aag ctc agc gg ^c ctc ttt gg ^g gac act caa tcc aaa gac cca aag				2202
Thr	Lys	Leu	Ser	Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys
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				660
ccg gag gcc atc ctc ac ^g cca ctc at ^g cac aac gg ^c aag ctc gcc act				2250
Pro	Glu	Ala	Ile	Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr
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				670
				675
ccc ggc aac ac ^g gg ^c aag at ^g ctc att aaa gca gac cag cac cac ct ^g				2298
Pro	Gly	Asn	Thr	Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu
				680
				685
				690
				695
gac ct ^g ac ^g gg ^c ctc ccc acc cca gag tca acc cca ac ^g ct ^g cag cag				2346
Asp	Leu	Thr	Ala	Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln
				700
				705
				710
aag cg ^g gaa ccc agc cg ^c gg ^c acc cg ^c gag tgg gag agg aac cag aac				2394
Lys	Arg	Glu	Pro	Ser Arg Gly Thr Arg Glu Trp Glu Arg Asn Gln Asn
				715
				720
				725
ctc atc aat gg ^c tgc aca aag gac at ^g ccc ccc at ^g gg ^c tcc cct gt ^g				2442
Leu	Ile	Asn	Ala	Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val
				730
				735
				740
att ccc ac ^g gac ct ^g ccc ct ^g cg ^c gg ^c tcc ccc agc cac atc ccc ag ^c				2490
Ile	Pro	Thr	Asp	Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser
				745
				750
				755
gt ^g gt ^g gtc ct ^g ccc atc ac ^g cag cag gg ^c tac cag cat gag tac gt ^g				2538
Val	Val	Val	Leu	Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val
				760
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				770
				775
gac cag ccc aaa at ^g agc gag gt ^g gg ^c cag at ^g g ^c ct ^g gag gac cag				2586
Asp	Gln	Pro	Lys	Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln
				780
				785
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gcc gcc aca ct ^g gag tat aag acc atc aag gaa cat ctc agc agc aag				2634
Ala	Ala	Thr	Leu	Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys
				795
				800
				805
agt ccc aac cat gg ^c gt ^g aac ctt gt ^g gag aac ct ^g gac agc ct ^g ccc				2682
Ser	Pro	Asn	His	Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro
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				815
				820
ccc aaa gtt cca cag cg ^g gag gg ^c tcc ct ^g ggt ccc cc ^g gga gg ^c tcc				2730
Pro	Lys	Val	Pro	Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser
				825
				830
				835

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Leu Ser Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser	
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Ser Tyr Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr	
860 865 870	
aga agc cac ctg acc acc tac tct cat cag aag caa cac taacccgac	2875
Arg Ser His Leu Thr Thr Tyr Ser His Gln Lys Gln His	
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aattcanctc tgacttcaaa gggaccagag ctggcagg ggagacaacc cgccgcccgc	2935
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Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr	
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Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys	
100 105 110	

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
115 120 125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
130 135 140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145 150 155 160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
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Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
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Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
195 200 205

Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
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Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
225 230 235 240

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
245 250 255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
260 265 270

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
275 280 285

Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
290 295 300

Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
305 310 315 320

Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
325 330 335

Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
340 345 350

Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
355 360 365

Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
370 375 380

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
385 390 395 400

Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
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Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
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Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
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Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
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Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
465 470 475 480

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515 520 525

Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
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Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
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Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
565 570 575

Gly Val Ile Arg Glu Ser Tyr Leu Lys Gly His Asp Gln Leu Val Pro
580 585 590

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595 600 605

Val Phe Ser Gly Ile Thr Val Tyr Cys Val Cys Asp His Arg Arg Lys
610 615 620

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625 630 635 640

Arg Gly Ser Met Ser Ser Val Thr Lys Leu Ser Gly Leu Phe Gly Asp
645 650 655

Thr Gln Ser Lys Asp Pro Lys Pro Glu Ala Ile Leu Thr Pro Leu Met
660 665 670

His Asn Gly Lys Leu Ala Thr Pro Gly Asn Thr Ala Lys Met Leu Ile
675 680 685

Lys Ala Asp Gln His His Leu Asp Leu Thr Ala Leu Pro Thr Pro Glu
690 695 700

Ser Thr Pro Thr Leu Gln Gln Lys Arg Glu Pro Ser Arg Gly Thr Arg
705 710 715 720

Glu Trp Glu Arg Asn Gln Asn Leu Ile Asn Ala Cys Thr Lys Asp Met
725 730 735

Pro Pro Met Gly Ser Pro Val Ile Pro Thr Asp Leu Pro Leu Arg Ala
740 745 750

Ser Pro Ser His Ile Pro Ser Val Val Val Leu Pro Ile Thr Gln Gln
755 760 765

Gly Tyr Gln His Glu Tyr Val Asp Gln Pro Lys Met Ser Glu Val Ala
770 775 780

Gln Met Ala Leu Glu Asp Gln Ala Ala Thr Leu Glu Tyr Lys Thr Ile
785 790 795 800

Lys Glu His Leu Ser Ser Lys Ser Pro Asn His Gly Val Asn Leu Val
805 810 815

Glu Asn Leu Asp Ser Leu Pro Pro Lys Val Pro Gln Arg Glu Ala Ser
820 825 830

Leu Gly Pro Pro Gly Ala Ser Leu Ser Gln Thr Gly Leu Ser Lys Arg
835 840 845

Leu Glu Met His His Ser Ser Ser Tyr Gly Val Asp Tyr Lys Arg Ser
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Tyr Pro Thr Asn Ser Leu Thr Arg Ser His Leu Thr Thr Tyr Ser His
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Met Ile Met Asn Ile Ala Gln Ser Asn Ala Val
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Ile Ser Gln Trp Leu Phe Met Ile Arg Ser Phe His Cys Met Leu Thr
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Leu Phe Met Glu Lys Cys Asn Lys Cys Gln Asn Ile Asn Gln Lys Phe	
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Leu Leu Gln Ile Ile Ala Lys Asn Leu Phe Ser Thr Pro Leu Leu Glu	
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Tyr Ser Lys Lys Phe Arg Val Ile Thr Arg Phe Gly Val Cys His Phe	
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Trp Ala Glu Arg Asp Phe Arg Phe Gln Arg Asn Lys Leu Cys Phe Thr	
80 85 90	
ggg agc cgg tgt tgt cca tgt agg ttc agg gct ttt aga aat ttt agg	458
Gly Ser Arg Cys Cys Pro Cys Arg Phe Arg Ala Phe Arg Asn Phe Arg	
95 100 105	
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Cys Asn Cys Ser Gly Thr Cys Gly Ser Phe Arg Phe Gly Ser Trp Arg	
110 115 120	
ttt ggg ccg ggg gcg tcg ttt agg tgt aga agg gat aga tgt agt ttg	554
Phe Gly Pro Gly Ala Ser Phe Arg Cys Arg Arg Asp Arg Cys Ser Leu	
125 130 135	
ctg ggg agc agg tgt cgt agg ctg cat ttc tgg act ggt aaa gat ttc	602
Leu Gly Ser Arg Cys Arg Arg Leu His Phe Trp Thr Gly Lys Asp Phe	
140 145 150 155	
cag ttt ttg agg aac aaa tgg tgt ttc act tgg agc cag tgt tgc cct	650
Gln Phe Leu Arg Asn Lys Trp Cys Phe Thr Trp Ser Gln Cys Cys Pro	
160 165 170	
tgg ctg ttc aag agt tct aga agt ttt agg tgg gat aga atc cag aat	698
Trp Leu Phe Lys Ser Ser Arg Ser Phe Arg Trp Asp Arg Ile Gln Asn	
175 180 185	
acg atc act tgt tgc tgg gta gga atc tgatatctca ggctcatcta	745
Thr Ile Thr Cys Cys Trp Val Gly Ile	
190 195	
atgtttagg gcttgagaaa acatcataag ttgcagttt aggctgcaga actttggaat	805
ctttccagaa ttccctgagg caaaaacacc cttccctttt gaaaaaccta g	856

<210> 8
 <211> 196
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ile Met Asn Ile Ala Gln Ser Asn Ala Val Ile Ser Gln Trp Leu
 1 5 10 15

Phe Met Ile Arg Ser Phe His Cys Met Leu Thr Leu Phe Met Glu Lys
20 25 30

Cys Asn Lys Cys Gln Asn Ile Asn Gln Lys Phe Leu Leu Gln Ile Ile
35 40 45

Ala Lys Asn Leu Phe Ser Thr Pro Leu Leu Glu Tyr Ser Lys Lys Phe
50 55 60

Arg Val Ile Thr Arg Phe Gly Val Cys His Phe Trp Ala Glu Arg Asp
65 70 75 80

Phe Arg Phe Gln Arg Asn Lys Leu Cys Phe Thr Gly Ser Arg Cys Cys
85 90 95

Pro Cys Arg Phe Arg Ala Phe Arg Asn Phe Arg Cys Asn Cys Ser Gly
100 105 110

Thr Cys Gly Ser Phe Arg Phe Gly Ser Trp Arg Phe Gly Pro Gly Ala
115 120 125

Ser Phe Arg Cys Arg Arg Asp Arg Cys Ser Leu Leu Gly Ser Arg Cys
130 135 140

Arg Arg Leu His Phe Trp Thr Gly Lys Asp Phe Gln Phe Leu Arg Asn
145 150 155 160

Lys Trp Cys Phe Thr Trp Ser Gln Cys Cys Pro Trp Leu Phe Lys Ser
165 170 175

Ser Arg Ser Phe Arg Trp Asp Arg Ile Gln Asn Thr Ile Thr Cys Cys
180 185 190

Trp Val Gly Ile
195

<210> 9
<211> 2341
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (215)..(2173)

<400> 9
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ccgtggagaa agcttaagga caccacgcca gtgcgttcct gccttccttc cgagatggaa 120
agaggagctc ctagctcact taagccgggg tagggcttgt tctcctttcc gagccaaaat 180
cccaggcgat ggtgaattat gaacgtgcca cacc atg aag ctc ttg tgg cag gta 235
Met Lys Leu Leu Trp Gln Val

act gtg cac cac cac acc tgg aat gcc atc ctg ctc ccg ttc gtc tac	283
Thr Val His His His Thr Trp Asn Ala Ile Leu Leu Pro Phe Val Tyr	
10 15 20	
ctc acg gcg caa gtg tgg att ctg tgt gca gcc atc gct gct gcc gcc	331
Leu Thr Ala Gln Val Trp Ile Leu Cys Ala Ala Ala Ala Ala Ala	
25 30 35	
tca gcc ggg ccc cag aac tgc ccc tcc gtc tgc tcg tgc agt aac cag	379
Ser Ala Gly Pro Gln Asn Cys Pro Ser Val Cys Ser Cys Ser Asn Gln	
40 45 50 55	
ttc agc aag gtg gtg tgc acg cgc cgg ggc ctc tcc gag gtc ccg cag	427
Phe Ser Lys Val Val Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln	
60 65 70	
ggt att ccc tcg aac acc cgg tac ctc aac ctc atg gag aac aac atc	475
Gly Ile Pro Ser Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile	
75 80 85	
cag atg atc cag gcc gac acc ttc cgc cac ctc cac cac ctg gag gtc	523
Gln Met Ile Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val	
90 95 100	
ctg cag ttg ggc agg aac tcc atc cgg cag att gag gtg ggg gcc ttc	571
Leu Gln Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe	
105 110 115	
aac ggc ctg gcc agc ctc agc acc ctg gag ctg ttc gac aac tgg ctg	619
Asn Gly Leu Ala Ser Leu Ser Thr Leu Glu Leu Phe Asp Asn Trp Leu	
120 125 130	
aca gtc atc cct agc ggg gcc ttt gaa tac ctg tcc aag ctg cgg gag	667
Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg Glu	
140 145 150	
ctc tgg ctt cgc aac aac ccc atc gaa agc atc ccc tct tac gcc ttc	715
Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr Ala Phe	
155 160 165	
aac cgg gtg ccc tcc ctc atg cgc ctg gac ttg ggg gag ctc aag aag	763
Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu Leu Lys Lys	
170 175 180	
ctg gag tat atc tct gag gga gct ttt gag ggg ctg ttc aac ctc aag	811
Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu Phe Asn Leu Lys	
185 190 195	
tat ctg aac ttg ggc atg tgc aac att aaa gac atg ccc aat ctc acc	859
Tyr Leu Asn Leu Gly Met Cys Asn Ile Lys Asp Met Pro Asn Leu Thr	
200 205 210 215	
ccc ctg gtg ggg ctg gag gag ctg gag atg tca ggg aac cac ttc cct	907
Pro Leu Val Gly Leu Glu Glu Leu Glu Met Ser Gly Asn His Phe Pro	
220 225 230	

gag atc agg cct ggc tcc ttc cat ggc ctg agc tcc ctc aag aag ctc		955	
Glu Ile Arg Pro Gly Ser Phe His Gly Leu Ser Ser Leu Lys Lys Leu			
235	240	245	
tgg gtc atg aac tca cag gtc agc ctg att gag cgg aat gct ttt gac		1003	
Trp Val Met Asn Ser Gln Val Ser Leu Ile Glu Arg Asn Ala Phe Asp			
250	255	260	
ggg ctg gct tca ctt gtg gaa ctc aac ttg gcc cac aat aac ctc tct		1051	
Gly Leu Ala Ser Leu Val Glu Leu Asn Leu Ala His Asn Asn Leu Ser			
265	270	275	
tct ttg ccc cat gac ctc ttt acc ccg ctg agg tac ctg gtg gag ttg		1099	
Ser Leu Pro His Asp Leu Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu			
280	285	290	295
cat cta cac cac aac cct tgg aac tgt gat tgt gac att ctg tgg cta		1147	
His Leu His His Asn Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu			
300	305	310	
gcc tgg tgg ctt cga gag tat ata ccc acc aat tcc acc tgc tgt ggc		1195	
Ala Trp Trp Leu Arg Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly			
315	320	325	
cgc tgt cat gct ccc atg cac atg cga ggc cgc tac ctc gtg gag gtg		1243	
Arg Cys His Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val			
330	335	340	
gac cag gcc tcc ttc cag tgc tct gcc ccc ttc atc atg gac gca cct		1291	
Asp Gln Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro			
345	350	355	
cga gac ctc aac att tct gag ggt cgg atg gca gaa ctt aag tgt cgg		1339	
Arg Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg			
360	365	370	375
act ccc cct atg tcc tcc gtg aag tgg ttg ctg ccc aat ggg aca gtg		1387	
Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr Val			
380	385	390	
ctc agc cac gcc tcc cgc cac cca agg atc tct gtc ctc aac gac ggc		1435	
Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn Asp Gly			
395	400	405	
acc ttg aac ttt tcc cac gtg ctg ctt tca gac act ggg gtg tac aca		1483	
Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly Val Tyr Thr			
410	415	420	
tgc atg ggg acc aat gtt gca ggc aac tcc aac gcc tcg gcc tac ctc		1531	
Cys Met Gly Thr Asn Val Ala Gly Asn Ser Asn Ala Ser Ala Tyr Leu			
425	430	435	
aat ggg agc acg gct gag ctt aac acc tcc aac tac agc ttc ttc acc		1579	
Asn Gly Ser Thr Ala Glu Leu Asn Thr Ser Asn Tyr Ser Phe Phe Thr			
440	445	450	455

aca gga aca ggg gag acc acg gag atc tcg cct gag gac aca acg cga	460	465	470	1627
Thr Gly Thr Gly Glu Thr Thr Glu Ile Ser Pro Glu Asp Thr Thr Arg				
aag tac aag cct cct acc acg tcc act ggt tac cag ccg gca tat	475	480	485	1675
Lys Tyr Lys Pro Val Pro Thr Thr Ser Thr Gly Tyr Gln Pro Ala Tyr				
acc acc tct acc acg gtg ctc att cag act acc cgt gtg ccc aag cag	490	495	500	1723
Thr Thr Ser Thr Thr Val Leu Ile Gln Thr Thr Arg Val Pro Lys Gln				
gtg gca gta ccc gcg aca gac acc act gac aag atg cag acc agc ctg	505	510	515	1771
Val Ala Val Pro Ala Thr Asp Thr Asp Lys Met Gln Thr Ser Leu				
gat gaa gtc atg aag acc acc aag atc atc att ggc tgc ttt gtg gca	520	525	530	1819
Asp Glu Val Met Lys Thr Thr Lys Ile Ile Gly Cys Phe Val Ala				
gtg act ctg cta gct gcc gcc atg ttg att gtc ttc tat aaa ctt cgt	540	545	550	1867
Val Thr Leu Ala Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg				
aag cgg cac cag cag cgg agt aca gtc aca gcc gcc cgg act gtt gag	555	560	565	1915
Lys Arg His Gln Gln Arg Ser Thr Val Thr Ala Ala Arg Thr Val Glu				
ata atc cag gtg gac gaa gac atc cca gca gca aca tcc gca gca gca	570	575	580	1963
Ile Ile Gln Val Asp Glu Asp Ile Pro Ala Ala Thr Ser Ala Ala Ala				
aca gca gct ccg tcc ggt gta tca ggt gaa ggg gca gta gtg ctg ccc	585	590	595	2011
Thr Ala Ala Pro Ser Gly Val Ser Gly Glu Gly Ala Val Val Leu Pro				
aca att cat gac cat att aac tac aac acc tac aaa cca gca cat ggg	600	605	610	2059
Thr Ile His Asp His Ile Asn Tyr Asn Thr Tyr Lys Pro Ala His Gly				
gcc cac tgg aca gaa aac agc ctg ggg aac tct ctg cac ccc aca gtc	620	625	630	2107
Ala His Trp Thr Glu Asn Ser Leu Gly Asn Ser Leu His Pro Thr Val				
acc act atc tct gaa cct tat ata att cag acc cat acc aag gac aag	635	640	645	2155
Thr Thr Ile Ser Glu Pro Tyr Ile Ile Gln Thr His Thr Lys Asp Lys				
gta cag gaa act caa ata tgactccct cccccaaaaa acttataaaaa	650			2203
Val Gln Glu Thr Gln Ile				
tgcaatagaa tgcacacaaa gacagcaact tttgtacaga gtggggagag actttttctt				2263
gtatatgctt atatattaag tctatggct ggtaaaaaaa aacagattat attaaaattt				2323
aaagacaaaa agtcaaaa				2341

<210> 10
<211> 653
<212> PRT
<213> Homo sapiens

<400> 10
Met Lys Leu Leu Trp Gln Val Thr Val His His His Thr Trp Asn Ala
1 5 10 15
Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile Leu Cys
20 25 30
Ala Ala Ile Ala Ala Ala Ser Ala Gly Pro Gln Asn Cys Pro Ser
35 40 45
Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val Cys Thr Arg Arg
50 55 60
Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser Asn Thr Arg Tyr Leu
65 70 75 80
Asn Leu Met Glu Asn Asn Ile Gln Met Ile Gln Ala Asp Thr Phe Arg
85 90 95
His Leu His His Leu Glu Val Leu Gln Leu Gly Arg Asn Ser Ile Arg
100 105 110
Gln Ile Glu Val Gly Ala Phe Asn Gly Leu Ala Ser Leu Ser Thr Leu
115 120 125
Glu Leu Phe Asp Asn Trp Leu Thr Val Ile Pro Ser Gly Ala Phe Glu
130 135 140
Tyr Leu Ser Lys Leu Arg Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu
145 150 155 160
Ser Ile Pro Ser Tyr Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu
165 170 175
Asp Leu Gly Glu Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe
180 185 190
Glu Gly Leu Phe Asn Leu Lys Tyr Leu Asn Leu Gly Met Cys Asn Ile
195 200 205
Lys Asp Met Pro Asn Leu Thr Pro Leu Val Gly Leu Glu Glu Leu Glu
210 215 220
Met Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly Ser Phe His Gly
225 230 235 240
Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser Gln Val Ser Leu
245 250 255
Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu Val Glu Leu Asn

260

265

270

Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp Leu Phe Thr Pro
 275 280 285

Leu Arg Tyr Leu Val Glu Leu His Leu His His Asn Pro Trp Asn Cys
 290 295 300

Asp Cys Asp Ile Leu Trp Leu Ala Trp Trp Leu Arg Glu Tyr Ile Pro
 305 310 315 320

Thr Asn Ser Thr Cys Cys Gly Arg Cys His Ala Pro Met His Met Arg
 325 330 335

Gly Arg Tyr Leu Val Glu Val Asp Gln Ala Ser Phe Gln Cys Ser Ala
 340 345 350

Pro Phe Ile Met Asp Ala Pro Arg Asp Leu Asn Ile Ser Glu Gly Arg
 355 360 365

Met Ala Glu Leu Lys Cys Arg Thr Pro Pro Met Ser Ser Val Lys Trp
 370 375 380

Leu Leu Pro Asn Gly Thr Val Leu Ser His Ala Ser Arg His Pro Arg
 385 390 395 400

Ile Ser Val Leu Asn Asp Gly Thr Leu Asn Phe Ser His Val Leu Leu
 405 410 415

Ser Asp Thr Gly Val Tyr Thr Cys Met Gly Thr Asn Val Ala Gly Asn
 420 425 430

Ser Asn Ala Ser Ala Tyr Leu Asn Gly Ser Thr Ala Glu Leu Asn Thr
 435 440 445

Ser Asn Tyr Ser Phe Phe Thr Thr Gly Thr Gly Glu Thr Thr Glu Ile
 450 455 460

Ser Pro Glu Asp Thr Thr Arg Lys Tyr Lys Pro Val Pro Thr Thr Ser
 465 470 475 480

Thr Gly Tyr Gln Pro Ala Tyr Thr Ser Thr Thr Val Leu Ile Gln
 485 490 495

Thr Thr Arg Val Pro Lys Gln Val Ala Val Pro Ala Thr Asp Thr Thr
 500 505 510

Asp Lys Met Gln Thr Ser Leu Asp Glu Val Met Lys Thr Thr Lys Ile
 515 520 525

Ile Ile Gly Cys Phe Val Ala Val Thr Leu Leu Ala Ala Ala Met Leu
 530 535 540

Ile Val Phe Tyr Lys Leu Arg Lys Arg His Gln Gln Arg Ser Thr Val
 545 550 555 560

Thr Ala Ala Arg Thr Val Glu Ile Ile Gln Val Asp Glu Asp Ile Pro

565

570

575

Ala Ala Thr Ser Ala Ala Ala Thr Ala Ala Pro Ser Gly Val Ser Gly
580 585 590

Glu Gly Ala Val Val Leu Pro Thr Ile His Asp His Ile Asn Tyr Asn
595 600 605

Thr Tyr Lys Pro Ala His Gly Ala His Trp Thr Glu Asn Ser Leu Gly
610 615 620

Asn Ser Leu His Pro Thr Val Thr Ile Ser Glu Pro Tyr Ile Ile
625 630 635 640

Gln Thr His Thr Lys Asp Lys Val Gln Glu Thr Gln Ile
645 650

<210> 11
<211> 2607
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (215)..(1984)

<400> 11
cacttccccc ttttgttaat taaaactaag aagtcggaat gggAACGAGG tgcccaGCTC 60
ccgtggagaa agcttaagga caccacGCCA gtgcTTTcCT gcTTcCTTC cgAGATGGAA 120
agaggAGCTC ctAGCTCact taAGCCGGGG tagggCTGgt tCTCCTTCC gagCCAAAAT 180
cccAGGCGat ggtGAATTAT gaacgtGCCA cacc atg aag ctc ttg tgg cag gta 235
Met Lys Leu Leu Trp Gln Val
1 5

act gtg cac cac cac acc tgg aat gcc atc ctg ctc ccg ttc gtc tac 283
Thr Val His His His Thr Trp Asn Ala Ile Leu Leu Pro Phe Val Tyr
10 15 20

ctc acg gcg caa gtg tgg att ctg tgt gca gcc atc gct gct gcc gcc 331
Leu Thr Ala Gln Val Trp Ile Leu Cys Ala Ala Ile Ala Ala Ala
25 30 35

tca gcc ggg ccc cag aac tgc ccc tcc gtc tgc tcg tgc agt aac cag 379
Ser Ala Gly Pro Gln Asn Cys Pro Ser Val Cys Ser Cys Ser Asn Gln
40 45 50 55

ttc agc aag gtg gtg tgc acg cgc cgg ggc ctc tcc gag gtc ccg cag 427
Phe Ser Lys Val Val Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln
60 65 70

ggt att ccc tcg aac acc cgg tac ctc aac ctc atg gag aac aac atc 475
Gly Ile Pro Ser Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile

75

80

85

cag atg atc cag gcc gac acc ttc cgc cac ctc cac cac ctg gag gtc			523
Gln Met Ile Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val			
90	95	100	
ctg cag ttg ggc agg aac tcc atc cgg cag att gag gtg ggg gcc ttc			571
Leu Gln Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe			
105	110	115	
aac ggc ctg gcc agc ctc agc acc ctg gag ctg ttc gac aac tgg ctg			619
Asn Gly Leu Ala Ser Leu Ser Thr Leu Glu Leu Phe Asp Asn Trp Leu			
120	125	130	135
aca gtc atc cct agc ggg gcc ttt gaa tac ctg tcc aag ctg cgg gag			667
Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg Glu			
140	145	150	
ctc tgg ctt cgc aac aac ccc atc gaa agc atc ccc tct tac gcc ttc			715
Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr Ala Phe			
155	160	165	
aac cgg gtg ccc tcc ctc atg cgc ctg gac ttg ggg gag ctc aag aag			763
Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu Leu Lys Lys			
170	175	180	
ctg gag tat atc tct gag gga gct ttt gag ggg ctg ttc aac ctc aag			811
Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu Phe Asn Leu Lys			
185	190	195	
tat ctg aac ttg ggc atg tgc aac att aaa gac atg ccc aat ctc acc			859
Tyr Leu Asn Leu Gly Met Cys Asn Ile Lys Asp Met Pro Asn Leu Thr			
200	205	210	215
ccc ctg gtg ggg ctg gag gag ctg gag atg tca ggg aac cac ttc cct			907
Pro Leu Val Gly Leu Glu Glu Leu Glu Met Ser Gly Asn His Phe Pro			
220	225	230	
gag atc agg cct ggc tcc ttc cat ggc ctg agc tcc ctc aag aag ctc			955
Glu Ile Arg Pro Gly Ser Phe His Gly Leu Ser Ser Leu Lys Lys Leu			
235	240	245	
tgg gtc atg aac tca cag gtc agc ctg att gag cgg aat gct ttt gac			1003
Trp Val Met Asn Ser Gln Val Ser Leu Ile Glu Arg Asn Ala Phe Asp			
250	255	260	
ggg ctg gct tca ctt gtg gaa ctc aac ttg gcc cac aat aac ctc tct			1051
Gly Leu Ala Ser Leu Val Glu Leu Asn Leu Ala His Asn Asn Leu Ser			
265	270	275	
tct ttg ccc cat gac ctc ttt acc ccg ctg agg tac ctg gtg gag ttg			1099
Ser Leu Pro His Asp Leu Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu			
280	285	290	295
cat cta cac cac aac cct tgg aac tgt gat tgt gac att ctg tgg cta			1147
His Leu His His Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu			
300	305	310	

gcc tgg tgg ctt cga gag tat ata ccc acc aat tcc acc tgc tgt ggc Ala Trp Trp Leu Arg Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly 315 320 325	1195
cgc tgt cat gct ccc atg cac atg cga ggc cgc tac ctc gtg gag gtg Arg Cys His Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val 330 335 340	1243
gac cag gcc tcc ttc cag tgc tct gcc ccc ttc atc atg gac gca cct Asp Gln Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro 345 350 355	1291
cga gac ctc aac att tct gag ggt cgg atg gca gaa ctt aag tgt cgg Arg Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg 360 365 370 375	1339
act ccc cct atg tcc tcc gtg aag tgg ttg ctg ccc aat ggg aca gtg Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr Val 380 385 390	1387
ctc agc cac gcc tcc cgc cac cca agg atc tct gtc ctc aac gac ggc Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn Asp Gly 395 400 405	1435
acc ttg aac ttt tcc cac gtg ctg ctt tca gac act ggg gtg tac aca Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly Val Tyr Thr 410 415 420	1483
tgc atg ggg acc aat gtt gca ggc aac tcc aac gcc tcg gcc tac ctc Cys Met Gly Thr Asn Val Ala Gly Asn Ser Asn Ala Ser Ala Tyr Leu 425 430 435	1531
aat ggg agc acg gct gag ctt aac acc tcc aac tac agc ttc ttc acc Asn Gly Ser Thr Ala Glu Leu Asn Thr Ser Asn Tyr Ser Phe Phe Thr 440 445 450 455	1579
aca gga aca ggg gag acc acg gag atc tcg cct gag gac aca acg cga Thr Gly Thr Gly Glu Thr Thr Glu Ile Ser Pro Glu Asp Thr Thr Arg 460 465 470	1627
aag tac aag cct gtt cct acc acg tcc act ggt tac cag ccg gca tat Lys Tyr Lys Pro Val Pro Thr Thr Ser Thr Gly Tyr Gln Pro Ala Tyr 475 480 485	1675
acc acc tct acc acg gtg ctc att cag act acc cgt gtg ccc aag cag Thr Thr Ser Thr Thr Val Leu Ile Gln Thr Thr Arg Val Pro Lys Gln 490 495 500	1723
gtg gca gta ccc gcg aca gac acc act gac aag atg cag acc agc ctg Val Ala Val Pro Ala Thr Asp Thr Asp Lys Met Gln Thr Ser Leu 505 510 515	1771
gat gaa gtc atg aag acc acc aag atc atc att ggc tgc ttt gtg gca Asp Glu Val Met Lys Thr Thr Lys Ile Ile Gly Cys Phe Val Ala 520 525 530 535	1819

gtg act ctg cta gct gcc gcc atg ttg att gtc ttc tat aaa ctt cgt		1867
Val Thr Leu Leu Ala Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg		
540	545	550
aag cg ^g cac cag cag cg ^g agt aca gtc aca gcc gcc ccc aca ctg gag		1915
Lys Arg His Gln Gln Arg Ser Thr Val Thr Ala Ala Pro Thr Leu Glu		
555	560	565
aga aaa cac agg gac aaa aac aca cca caa aaa cac cca caa caa		1963
Arg Lys His Arg Asp Lys Asn Thr Pro Gln Gln Lys His Pro Gln Gln		
570	575	580
aaa caa cag ccc ccc ccg gta taacaggaaa gggcacaata gcgc ^{ccc} caca		2014
Lys Gln Gln Pro Pro Pro Val		
585	590	
aaacacaaca acataaaaaaa caaaacacac acaaaccagc acatggggcc cactggacag		2074
aaaacagcct ggggaactct gtgcacccca cagtcaccac tatctctgaa ccttatataa		2134
ttcagaccca taccaaggac aaggtacagg aaactcaat atgactcccc tcccccaaaa		2194
aacttataaa atgcaataga atgcacacaa agacagcaac ttttgtacag agtggggaga		2254
gacttttct tgtatatgct tatatattaa gtctatggc tggtaaaaaa aaacagatta		2314
tataaaatt taaagacaaa aagtcaaaac aaaaatattt tctaacttgt aagttctatt		2374
taaagggggt ggggggaaat cttgggaacg ttgtgggta caagccacaa gttaacttgc		2434
tatgctgcca gaagggattt ctggtaaag gttgaaattt ctgagataaa ataaactaaa		2494
acaacaaaca tccttaaaga ggtagggtgt gggctgctga aggggcaaga gggatagact		2554
gaatctgtca tttttagaag atgcttcata ggacacagga ctatccattt cta		2607

<210> 12
 <211> 590
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Lys Leu Leu Trp Gln Val Thr Val His His His Thr Trp Asn Ala
 1 5 10 15

Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile Leu Cys
 20 25 30

Ala Ala Ile Ala Ala Ala Ser Ala Gly Pro Gln Asn Cys Pro Ser
 35 40 45

Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val Cys Thr Arg Arg
 50 55 60

Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser Asn Thr Arg Tyr Leu
 65 70 75 80

Asn Leu Met Glu Asn Asn Ile Gln Met Ile Gln Ala Asp Thr Phe Arg
85 90 95

His Leu His His Leu Glu Val Leu Gln Leu Gly Arg Asn Ser Ile Arg
100 105 110

Gln Ile Glu Val Gly Ala Phe Asn Gly Leu Ala Ser Leu Ser Thr Leu
115 120 125

Glu Leu Phe Asp Asn Trp Leu Thr Val Ile Pro Ser Gly Ala Phe Glu
130 135 140

Tyr Leu Ser Lys Leu Arg Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu
145 150 155 160

Ser Ile Pro Ser Tyr Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu
165 170 175

Asp Leu Gly Glu Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe
180 185 190

Glu Gly Leu Phe Asn Leu Lys Tyr Leu Asn Leu Gly Met Cys Asn Ile
195 200 205

Lys Asp Met Pro Asn Leu Thr Pro Leu Val Gly Leu Glu Glu Leu Glu
210 215 220

Met Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly Ser Phe His Gly
225 230 235 240

Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser Gln Val Ser Leu
245 250 255

Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu Val Glu Leu Asn
260 265 270

Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp Leu Phe Thr Pro
275 280 285

Leu Arg Tyr Leu Val Glu Leu His Leu His His Asn Pro Trp Asn Cys
290 295 300

Asp Cys Asp Ile Leu Trp Leu Ala Trp Trp Leu Arg Glu Tyr Ile Pro
305 310 315 320

Thr Asn Ser Thr Cys Cys Gly Arg Cys His Ala Pro Met His Met Arg
325 330 335

Gly Arg Tyr Leu Val Glu Val Asp Gln Ala Ser Phe Gln Cys Ser Ala
340 345 350

Pro Phe Ile Met Asp Ala Pro Arg Asp Leu Asn Ile Ser Glu Gly Arg
355 360 365

Met Ala Glu Leu Lys Cys Arg Thr Pro Pro Met Ser Ser Val Lys Trp
370 375 380

Leu Leu Pro Asn Gly Thr Val Leu Ser His Ala Ser Arg His Pro Arg
385 390 395 400

Ile Ser Val Leu Asn Asp Gly Thr Leu Asn Phe Ser His Val Leu Leu
405 410 415

Ser Asp Thr Gly Val Tyr Thr Cys Met Gly Thr Asn Val Ala Gly Asn
420 425 430

Ser Asn Ala Ser Ala Tyr Leu Asn Gly Ser Thr Ala Glu Leu Asn Thr
435 440 445

Ser Asn Tyr Ser Phe Phe Thr Thr Gly Thr Gly Glu Thr Thr Glu Ile
450 455 460

Ser Pro Glu Asp Thr Thr Arg Lys Tyr Lys Pro Val Pro Thr Thr Ser
465 470 475 480

Thr Gly Tyr Gln Pro Ala Tyr Thr Ser Thr Thr Val Leu Ile Gln
485 490 495

Thr Thr Arg Val Pro Lys Gln Val Ala Val Pro Ala Thr Asp Thr Thr
500 505 510

Asp Lys Met Gln Thr Ser Leu Asp Glu Val Met Lys Thr Thr Lys Ile
515 520 525

Ile Ile Gly Cys Phe Val Ala Val Thr Leu Leu Ala Ala Ala Met Leu
530 535 540

Ile Val Phe Tyr Lys Leu Arg Lys Arg His Gln Gln Arg Ser Thr Val
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Thr Ala Ala Pro Thr Leu Glu Arg Lys His Arg Asp Lys Asn Thr Pro
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Gln Gln Lys His Pro Gln Gln Lys Gln Gln Pro Pro Pro Val
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<213> Homo sapiens

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<222> (22)
<223> an n may be any one of a or t or g or c

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 accgtttcag cctggccagc cctctggacc ccgaggttgg accctactgt gacacaccta 180
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 tttcagataa gccggtgcaa gaccgggtt tggtggtgac ggacctcaaa gctgagatg 360
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 atg tac tgg gct atg tca ctc cac cag tgg aac agc cat ggc tac gat 468
 Met Tyr Trp Ala Met Ser Leu His Gln Trp Asn Ser His Gly Tyr Asp
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 Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp
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 Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu
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 His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys
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 ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac tgg act tac gat 660
 Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp
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 85 90 95
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 Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val
 100 105 110
 gtg gag gtc tgg aac cag ctg cta agc cag aag cgc gtg ggc ctc atc 804
 Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile
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 cac atg ctc acc cac ttg gcc gag gct ctg cac cag gcc cgg ctg ctg 852
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 130 135 140
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 Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu
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 Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp
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Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly																																																							
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190																																																							
cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc cag gtc ctg gac	1044																																																						
Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp																																																							
195	200	205		ccg aag tcc aag tgg cga aac aaa atc ctc ctg ggg ctc aac ttc tat	1092	Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr		210	215	220		ggt atg gac tac gcg acc tcc aag gat gcc cgt gag cct gtt gtc ggg	1140	Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly		225	230	235	240	gcc agg tac atg cag aca ctg aag tct gca ttc gta ctc tta gca aac	1188	Ala Arg Tyr Met Gln Thr Leu Lys Ser Ala Phe Val Leu Leu Ala Asn		245	250	255		ttg gaa aat ttg agg cga aat tct tca aat aaa aaa aaa aaa aaa aaa	1236	Leu Glu Asn Leu Arg Arg Asn Ser Ser Asn Lys Lys Lys Lys Lys Lys		260	265	270		aat ttt ttc tgt ttc ttc tct tct gtc ttc tcg ttt gga gac cac aaa	1284	Asn Phe Phe Cys Phe Phe Ser Ser Val Phe Ser Phe Gly Asp His Lys		275	280	285		cac tagatccatt gaatttgcac cacagctcac gaatacacacct tttacctttt gga	1340	His									
205																																																							
ccg aag tcc aag tgg cga aac aaa atc ctc ctg ggg ctc aac ttc tat	1092																																																						
Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr																																																							
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220																																																							
ggt atg gac tac gcg acc tcc aag gat gcc cgt gag cct gtt gtc ggg	1140																																																						
Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly																																																							
225	230	235	240	gcc agg tac atg cag aca ctg aag tct gca ttc gta ctc tta gca aac	1188	Ala Arg Tyr Met Gln Thr Leu Lys Ser Ala Phe Val Leu Leu Ala Asn		245	250	255		ttg gaa aat ttg agg cga aat tct tca aat aaa aaa aaa aaa aaa aaa	1236	Leu Glu Asn Leu Arg Arg Asn Ser Ser Asn Lys Lys Lys Lys Lys Lys		260	265	270		aat ttt ttc tgt ttc ttc tct tct gtc ttc tcg ttt gga gac cac aaa	1284	Asn Phe Phe Cys Phe Phe Ser Ser Val Phe Ser Phe Gly Asp His Lys		275	280	285		cac tagatccatt gaatttgcac cacagctcac gaatacacacct tttacctttt gga	1340	His																									
235	240																																																						
gcc agg tac atg cag aca ctg aag tct gca ttc gta ctc tta gca aac	1188																																																						
Ala Arg Tyr Met Gln Thr Leu Lys Ser Ala Phe Val Leu Leu Ala Asn																																																							
245	250	255		ttg gaa aat ttg agg cga aat tct tca aat aaa aaa aaa aaa aaa aaa	1236	Leu Glu Asn Leu Arg Arg Asn Ser Ser Asn Lys Lys Lys Lys Lys Lys		260	265	270		aat ttt ttc tgt ttc ttc tct tct gtc ttc tcg ttt gga gac cac aaa	1284	Asn Phe Phe Cys Phe Phe Ser Ser Val Phe Ser Phe Gly Asp His Lys		275	280	285		cac tagatccatt gaatttgcac cacagctcac gaatacacacct tttacctttt gga	1340	His																																	
255																																																							
ttg gaa aat ttg agg cga aat tct tca aat aaa aaa aaa aaa aaa aaa	1236																																																						
Leu Glu Asn Leu Arg Arg Asn Ser Ser Asn Lys Lys Lys Lys Lys Lys																																																							
260	265	270		aat ttt ttc tgt ttc ttc tct tct gtc ttc tcg ttt gga gac cac aaa	1284	Asn Phe Phe Cys Phe Phe Ser Ser Val Phe Ser Phe Gly Asp His Lys		275	280	285		cac tagatccatt gaatttgcac cacagctcac gaatacacacct tttacctttt gga	1340	His																																									
270																																																							
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Asn Phe Phe Cys Phe Phe Ser Ser Val Phe Ser Phe Gly Asp His Lys																																																							
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285																																																							
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<210> 14
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Met Tyr Trp Ala Met Ser Leu His Gln Trp Asn Ser His Gly Tyr Asp																																	
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10	15																																
Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp																																	
20	25	30		Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu		35	40	45		His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys		50	55	60		Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp		65	70	75	80	Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser		85	90	95							
30																																	
Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu																																	
35	40	45		His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys		50	55	60		Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp		65	70	75	80	Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser		85	90	95													
45																																	
His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys																																	
50	55	60		Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp		65	70	75	80	Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser		85	90	95																			
60																																	
Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp																																	
65	70	75	80	Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser		85	90	95																									
75	80																																
Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser																																	
85	90	95																															
95																																	

Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val
100 105 110

Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile
115 120 125

His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu
130 135 140

Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu
145 150 155 160

Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp
165 170 175

Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly
180 185 190

Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp
195 200 205

Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr
210 215 220

Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly
225 230 235 240

Ala Arg Tyr Met Gln Thr Leu Lys Ser Ala Phe Val Leu Leu Ala Asn
245 250 255

Leu Glu Asn Leu Arg Arg Asn Ser Ser Asn Lys Lys Lys Lys Lys Lys
260 265 270

Asn Phe Phe Cys Phe Phe Ser Ser Val Phe Ser Phe Gly Asp His Lys
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Met His Tyr Tyr Arg Tyr
1 5

tct aac gcc aag gtc agc tgc tgg tac aag tac ctc ctt ttc agc tac Ser Asn Ala Lys Val Ser Cys Trp Tyr Lys Tyr Leu Leu Phe Ser Tyr 10 15 20	161
aac atc atc ttc tgg ttg gct gga gtt gtc ttc ctt gga gtc ggg ttg Asn Ile Ile Phe Trp Leu Ala Gly Val Val Phe Leu Gly Val Gly Leu 25 30 35	209
tgg gca tgg agc gaa aag ggt gtg ctg tcc gac ctc acc aaa gtg acc Trp Ala Trp Ser Glu Lys Gly Val Leu Ser Asp Leu Thr Lys Val Thr 40 45 50	257
cgg atg cat gga atc gac cct gcg gtg ctg gtc ctg atg gtg ggc gcg Arg Met His Gly Ile Asp Pro Ala Val Leu Val Leu Met Val Gly Ala 55 60 65 70	305
gtg atg ttc acc ctg ggg ttc gcc ggc cgc gtg ggg gcg cgc agg gag Val Met Phe Thr Leu Gly Phe Ala Gly Arg Val Gly Ala Arg Arg Glu 75 80 85	353
aat atc tgc ttg ctc aac ttt ttc tgt ggc acc atc gtg ctc atc ttc Asn Ile Cys Leu Leu Asn Phe Phe Cys Gly Thr Ile Val Leu Ile Phe 90 95 100	401
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gtg agg gac cgg ttc cgg gag ttc gag agc aac atc aag tcc tac Val Arg Asp Arg Phe Arg Glu Phe Phe Glu Ser Asn Ile Lys Ser Tyr 120 125 130	497
cgg gac gat atc gat ctg caa aac ctc atc gac tcc ctt cag aaa gct Arg Asp Asp Ile Asp Leu Gln Asn Leu Ile Asp Ser Leu Gln Lys Ala 135 140 145 150	545
aac cag tgc tgt ggc gca tat ggc cct gaa gac tgg gac ctc aac gtc Asn Gln Cys Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val 155 160 165	593
tac ttc aat tgc agc ggt gcc agc tac agc cga gag aag tgc ggg gtc Tyr Phe Asn Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val 170 175 180	641
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cag tgt gga tat gat gtc agg att cag ctg aag agc aag tgg gat gag Gln Cys Gly Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu 200 205 210	737
tcc atc ttc acg aaa ggc tgc atc cag gcg ctg gaa agc tgg ctc ccg Ser Ile Phe Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro 215 220 225 230	785
cgg aac att tac att gtg gct ggc gtc ttc atc gcc atc tcg ctg ttg	833

Arg Asn Ile Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu			
235	240	245	
cag ata ttt ggc atc ttc ctg gca agg acg ctg atc tca gac atc gag	881		
Gln Ile Phe Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu			
250	255	260	
gca gtg aag acc ggc cat cac ttc tgaggagcag agttgaggga gccgagctga	935		
Ala Val Lys Thr Gly His His Phe			
265	270		
gccacgctgg gaggccagag cctttctctg ccatcagccc tacgtccaga gggagaggag	995		
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20	25	30	

Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val Leu Ser			
35	40	45	

Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Ala Val Leu			
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Val Leu Met Val Gly Ala Val Met Phe Thr Leu Gly Phe Ala Gly Arg			
65	70	75	80

Val Gly Ala Arg Arg Glu Asn Ile Cys Leu Leu Asn Phe Phe Cys Gly			
85	90	95	

Thr Ile Val Leu Ile Phe Phe Leu Glu Leu Ala Val Ala Val Leu Ala			
100	105	110	

Phe	Leu	Phe	Gln	Asp	Trp	Val	Arg	Asp	Arg	Phe	Arg	Glu	Phe	Phe	Glu
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Ser	Asn	Ile	Lys	Ser	Tyr	Arg	Asp	Asp	Ile	Asp	Leu	Gln	Asn	Leu	Ile
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Asp	Ser	Leu	Gln	Lys	Ala	Asn	Gln	Cys	Cys	Gly	Ala	Tyr	Gly	Pro	Glu
145							150					155			160
Asp	Trp	Asp	Leu	Asn	Val	Tyr	Phe	Asn	Cys	Ser	Gly	Ala	Ser	Tyr	Ser
						165					170			175	
Arg	Glu	Lys	Cys	Gly	Val	Pro	Phe	Ser	Cys	Cys	Val	Pro	Asp	Pro	Ala
						180					185			190	
Gln	Lys	Val	Val	Asn	Thr	Gln	Cys	Gly	Tyr	Asp	Val	Arg	Ile	Gln	Leu
						195					200			205	
Lys	Ser	Lys	Trp	Asp	Glu	Ser	Ile	Phe	Thr	Lys	Gly	Cys	Ile	Gln	Ala
						210					215			220	
Leu	Glu	Ser	Trp	Leu	Pro	Arg	Asn	Ile	Tyr	Ile	Val	Ala	Gly	Val	Phe
						225					230			235	
Ile	Ala	Ile	Ser	Leu	Leu	Gln	Ile	Phe	Gly	Ile	Phe	Leu	Ala	Arg	Thr
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Leu	Ile	Ser	Asp	Ile	Glu	Ala	Val	Lys	Thr	Gly	His	His	Phe		
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Gly Pro Leu Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu Pro Gly
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35 40 45 50

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agc ttc ggg cct gga gaa tgg gat gac cgg aaa gtg cga cac act ttt Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His Thr Phe 85 90 95	344
atc cga aag gtt tac tcc atc atc tcc ggg cag ctg ctc atc act ggg Ile Arg Lys Val Tyr Ser Ile Ile Ser Gly Gln Leu Leu Ile Thr Gly 100 105 110	392
gcc atc att gct atc ttc acc ttt ggg gaa cct gtc agc gcc ttt ggc Ala Ile Ile Ala Ile Phe Thr Phe Gly Glu Pro Val Ser Ala Phe Gly 115 120 125 130	440
agg aga aat gtg gct gtc tac tac gtg tcc tat gct gtc ttc agt gtc Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe Ser Val 135 140 145	488
acc tac ctg atc ctt gcc tgc tgc cag gga ccc aga cgc cgt ttc cca Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg Phe Pro 150 155 160	536
tgg aac atc att ctg ctg acc ctt ttt act ttt gcc atg ggc ttc atg Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly Phe Met 165 170 175	584
acg ggc acc att tcc agt atg tac caa acc aaa gcc gtc atc att gca Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile Ile Ala 180 185 190	632
atg atc atc act gcg gtg gta tcc att tca gtc acc atc ttc tgc ttt Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe Cys Phe 195 200 205 210	680
cag acc aag gtg gac ttc acc tcg tgc aca ggc ctc ttc tgt gtc ctg Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys Val Leu 215 220 225	728
gga att gtg ctc ctg gtg act ggg att gtc act agc att gtg ctc tac Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val Leu Tyr 230 235 240	776
ttc caa tac gtt tac tgg ctc cac atg ctc tat gct gct ctg ggg gcc Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu Gly Ala 245 250 255	824
att tgt ttc acc ctg ttc ctg gct tac gac aca cag ctg gtc ctg ggg Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val Leu Gly 260 265 270	872

aac	cg	a	g	c	a	c	a	c	a	t	c	a	g	g	a	c	t	a	c	a	g	920
Asn	Arg	Lys	His	Thr	Ile	Ser	Pro	Glu	Asp	Tyr	Ile	Thr	Gly	Ala	Leu							
275					280					285						290						
cag	att	tac	aca	gac	atc	atc	tac	atc	ttc	acc	ttt	gtg	ctg	cag	ctg	968						
Gln	Ile	Tyr	Thr	Asp	Ile	Ile	Tyr	Ile	Phe	Thr	Phe	Val	Leu	Gln	Leu							
					295				300						305							
atg	ggg	gat	cgc	aat	taaggagcaa	gccccat	tttc	tcacccgatc	ctgggctctc	1023												
Met	Gly	Asp	Arg	Asn																		
				310																		
ccttccaagc	tagagggctg	ggccctatga	ctgtggtctg	ggcttttaggc	ccctttcctt	1083																
ccccttgagt	aacatgccc	gttccctt	tgtcctggag	acaggtggcc	tctctggcta	1143																
tggatgtgt	ggtacttggt	ggggacggag	gagctaggga	ctaactgtt	ctcttggtgg	1203																
gcttggcagg	gactaggctg	aagatgtgtc	ttctccccgc	cacctactgt	atgacaccac	1263																
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ggaatatgaa	aggtagaagt	gacttcaagg	tcacgaggtt	cccctccac	ctctgtcaca	1383																
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cccgccctcc	tggacacata	ggccattatc	ctgtattcct	ttggcttggc	atcttttagc	1503																
ttaggaaggt	agaagagatc	tgtccccatg	ggtctccctg	cttcaatccc	ttcttgggttc	1563																
agtacat	gtattgttta	tctgggttag	ggatggggga	cagataatag	aacgagcaaa	1623																
gtacccata	caggccagca	tggAACAGCA	tctccctgg	gcttgctcct	ggcttgtgac	1683																
gctataagac	agagcaggcc	acatgtggcc	atctgctccc	cattctt	gaa agctgctggg	1743																
gcctccttgc	aggcttctgg	atcc				1767																

<210> 18
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Ser Asn Pro Ser Ala Pro Pro Pro Tyr Glu Asp Arg Asn Pro Leu
 1 5 10 15

Tyr Pro Gly Pro Leu Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu
 20 25 30

Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr Gly
 35 40 45

His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro
 50 55 60

Met	Asn	Tyr	Gly	Pro	Gly	His	Gly	Tyr	Asp	Gly	Glu	Glu	Arg	Ala	Val
65					70					75				80	
Ser	Asp	Ser	Phe	Gly	Pro	Gly	Glu	Trp	Asp	Asp	Arg	Lys	Val	Arg	His
						85				90				95	
Thr	Phe	Ile	Arg	Lys	Val	Tyr	Ser	Ile	Ile	Ser	Gly	Gln	Leu	Leu	Ile
					100				105				110		
Thr	Gly	Ala	Ile	Ile	Ala	Ile	Phe	Thr	Phe	Gly	Glu	Pro	Val	Ser	Ala
					115				120				125		
Phe	Gly	Arg	Arg	Asn	Val	Ala	Val	Tyr	Tyr	Val	Ser	Tyr	Ala	Val	Phe
					130				135			140			
Ser	Val	Thr	Tyr	Leu	Ile	Leu	Ala	Cys	Cys	Gln	Gly	Pro	Arg	Arg	Arg
					145				150			155			160
Phe	Pro	Trp	Asn	Ile	Ile	Leu	Leu	Thr	Leu	Phe	Thr	Phe	Ala	Met	Gly
					165				170				175		
Phe	Met	Thr	Gly	Thr	Ile	Ser	Ser	Met	Tyr	Gln	Thr	Lys	Ala	Val	Ile
					180				185			190			
Ile	Ala	Met	Ile	Ile	Thr	Ala	Val	Val	Ser	Ile	Ser	Val	Thr	Ile	Phe
					195				200			205			
Cys	Phe	Gln	Thr	Lys	Val	Asp	Phe	Thr	Ser	Cys	Thr	Gly	Leu	Phe	Cys
					210				215			220			
Val	Leu	Gly	Ile	Val	Leu	Leu	Val	Thr	Gly	Ile	Val	Thr	Ser	Ile	Val
					225				230			235			240
Leu	Tyr	Phe	Gln	Tyr	Val	Tyr	Trp	Leu	His	Met	Leu	Tyr	Ala	Ala	Leu
					245				250			255			
Gly	Ala	Ile	Cys	Phe	Thr	Leu	Phe	Leu	Ala	Tyr	Asp	Thr	Gln	Leu	Val
					260				265			270			
Leu	Gly	Asn	Arg	Lys	His	Thr	Ile	Ser	Pro	Glu	Asp	Tyr	Ile	Thr	Gly
					275				280			285			
Ala	Leu	Gln	Ile	Tyr	Thr	Asp	Ile	Ile	Tyr	Ile	Phe	Thr	Phe	Val	Leu
					290				295			300			
Gln	Leu	Met	Gly	Asp	Arg	Asn									
					305				310						

<210> 19
<211> 1686
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (372)..(1277)

<220>

<221> misc_feature

<222> (1490)..(1630)

<223> an n may be any one of a or t or g or c

<400> 19

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agtacttaaa aaatagaaaa ataaaatact gtacacccaa ataagctaga aaaatggaac 120

taagaaataa tatttgaat taatataaaa tgaagctaca gaaggcataa gtaagtccaa 180

atgttggctc tttgaaagac tattaaataa ttacacagaa agtctaataa agagaaaaga 240

gagaaaaaaa ctgtcagaat gctaccgaac tgtactgctt ctacagttag aacacggatc 300

tgacttgcg gcagcccaag tgtgacaagt gcaatgctgc ctatcctcac ctggctcacc 360

tgccatctgc c atg gca gac tca tcc ttc cgg ttt cct cgc aca tgg tgg 410

Met Ala Asp Ser Ser Phe Arg Phe Pro Arg Thr Trp Trp

1 5 10

cag tct gcg gag gat gtg cac aga gaa aag atc cag tta gac ctg gaa 458

Gln Ser Ala Glu Asp Val His Arg Glu Lys Ile Gln Leu Asp Leu Glu

15 20 25

gct gaa ttc tac ttc act cac cta att gtg atg ttc aag tcc ccc agg 506

Ala Glu Phe Tyr Phe Thr His Leu Ile Val Met Phe Lys Ser Pro Arg

30 35 40 45

ccg gct gcc atg gtg ctg gac cgc tcc cag gac ttt ggg aaa aca tgg 554

Pro Ala Ala Met Val Leu Asp Arg Ser Gln Asp Phe Gly Lys Thr Trp

50 55 60

aag cct tat aag tac ttt gcg act aac tgc tcc gct aca ttt ggc ctg 602

Lys Pro Tyr Lys Tyr Phe Ala Thr Asn Cys Ser Ala Thr Phe Gly Leu

65 70 75

gaa gat gat gtt gtc aag aag ggc gct att tgt act tct aaa tac tcc 650

Glu Asp Asp Val Val Lys Lys Gly Ala Ile Cys Thr Ser Lys Tyr Ser

80 85 90

agt cct ttt cca tgc act gga gga gag gtt att ttc aaa gct ttg tca 698

Ser Pro Phe Pro Cys Thr Gly Gly Glu Val Ile Phe Lys Ala Leu Ser

95 100 105

cca cca tac gat aca gag aac cct tac agt gcc aaa gtt cag gag cag 746

Pro Pro Tyr Asp Thr Glu Asn Pro Tyr Ser Ala Lys Val Gln Glu Gln

110 115 120 125

ctg aag atc acc aac ctt cgc gtg cag ctg ctg aaa cga cag tct tgt 794

Leu Lys Ile Thr Asn Leu Arg Val Gln Leu Leu Lys Arg Gln Ser Cys

130 135 140

ccc tgt cag aga aat gac ctg aac gaa gag cct caa cat ttt aca cac 842

Pro	Cys	Gln	Arg	Asn	Asp	Leu	Asn	Glu	Glu	Pro	Gln	His	Phe	Thr	His	
145						150							155			
tat gca atc tat gat ttc att gtc aag ggc agc tgc ttc tgc aat ggc															890	
Tyr	Ala	Ile	Tyr	Asp	Phe	Ile	Val	Lys	Gly	Ser	Cys	Phe	Cys	Asn	Gly	
160			165							170						
cac gct gat caa tgc ata cct gtt cat ggc ttc aga cct gtc aag gcc															938	
His	Ala	Asp	Gln	Cys	Ile	Pro	Val	His	Gly	Phe	Arg	Pro	Val	Lys	Ala	
175			180					185								
cca gga aca ttc cac atg gtc cat ggg aag tgt atg tgt aag cac aac															986	
Pro	Gly	Thr	Phe	His	Met	Val	His	Gly	Lys	Cys	Met	Cys	Lys	His	Asn	
190			195			200				205						
aca gca ggc agc cac tgc cag cac tgt gcc ccg tta tac aat gac cgg															1034	
Thr	Ala	Gly	Ser	His	Cys	Gln	His	Cys	Ala	Pro	Leu	Tyr	Asn	Asp	Arg	
210			215				220									
cca tgg gag gca gct gat ggc aaa acg ggg gct ccc aac gag tgc aga															1082	
Pro	Trp	Glu	Ala	Ala	Asp	Gly	Lys	Thr	Gly	Ala	Pro	Asn	Glu	Cys	Arg	
225			230				235									
acc tgc aag tgt aat ggg cat gct gat acc tgt cac ttc gac gtt aat															1130	
Thr	Cys	Lys	Cys	Asn	Gly	His	Ala	Asp	Thr	Cys	His	Phe	Asp	Val	Asn	
240			245			250										
gtg tgg gag gca tca ggg aat cgt agt ggt ggt gtc tgt gat gac tgt															1178	
Val	Trp	Glu	Ala	Ser	Gly	Asn	Arg	Ser	Gly	Gly	Val	Cys	Asp	Asp	Cys	
255			260			265										
cag cac aac aca gaa gga cag tat tgc cag agg tgc aag cca ggc ttc															1226	
Gln	His	Asn	Thr	Glu	Gly	Gln	Tyr	Cys	Gln	Arg	Cys	Lys	Pro	Gly	Phe	
270			275			280			285							
tat cgt gac ctg cgg aga ccc ttc tca gct cca gat gct tgc aaa cgt															1274	
Tyr	Arg	Asp	Leu	Arg	Arg	Pro	Phe	Ser	Ala	Pro	Asp	Ala	Cys	Lys	Arg	
290			295			300										
aag taacctgtgg tttccagaaa ataggctgat ttgtacaaga gatgaatctc															1327	
Lys																
tttatccctc attctgctaa cccaagagaa ggaggtcatt gaggttctga gataacacac															1387	
ttacagatat	cggtaattt	cttcattgat	aagaagcaag	aattttcaac	cattgggtga											1447
aaacagtata	atattcatca	aaagtaattt	cctttctcat	tctncataaa	gtaaaaaatta											1507
ttccctatac	gctgcatttt	gtaaacagg	atgactaata	gaaaaaaaaa	tgatgaanaa											1567
ggagactatt	taagaactta	agactacttg	ggagtagaaag	gtagacaata	atggactcan											1627
ctgatgaaat	aaaggtaagt	actggacttg	gaatatctt	accttacagg	gaacttaac											1686

<210> 20

<211> 302

<212> PRT

<213> Homo sapiens

<400> 20

Met Ala Asp Ser Ser Phe Arg Phe Pro Arg Thr Trp Trp Gln Ser Ala
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Glu Asp Val His Arg Glu Lys Ile Gln Leu Asp Leu Glu Ala Glu Phe
20 25 30

Tyr Phe Thr His Leu Ile Val Met Phe Lys Ser Pro Arg Pro Ala Ala
35 40 45

Met Val Leu Asp Arg Ser Gln Asp Phe Gly Lys Thr Trp Lys Pro Tyr
50 55 60

Lys Tyr Phe Ala Thr Asn Cys Ser Ala Thr Phe Gly Leu Glu Asp Asp
65 70 75 80

Val Val Lys Lys Gly Ala Ile Cys Thr Ser Lys Tyr Ser Ser Pro Phe
85 90 95

Pro Cys Thr Gly Gly Glu Val Ile Phe Lys Ala Leu Ser Pro Pro Tyr
100 105 110

Asp Thr Glu Asn Pro Tyr Ser Ala Lys Val Gln Glu Gln Leu Lys Ile
115 120 125

Thr Asn Leu Arg Val Gln Leu Leu Lys Arg Gln Ser Cys Pro Cys Gln
130 135 140

Arg Asn Asp Leu Asn Glu Glu Pro Gln His Phe Thr His Tyr Ala Ile
145 150 155 160

Tyr Asp Phe Ile Val Lys Gly Ser Cys Phe Cys Asn Gly His Ala Asp
165 170 175

Gln Cys Ile Pro Val His Gly Phe Arg Pro Val Lys Ala Pro Gly Thr
180 185 190

Phe His Met Val His Gly Lys Cys Met Cys Lys His Asn Thr Ala Gly
195 200 205

Ser His Cys Gln His Cys Ala Pro Leu Tyr Asn Asp Arg Pro Trp Glu
210 215 220

Ala Ala Asp Gly Lys Thr Gly Ala Pro Asn Glu Cys Arg Thr Cys Lys
225 230 235 240

Cys Asn Gly His Ala Asp Thr Cys His Phe Asp Val Asn Val Trp Glu
245 250 255

Ala Ser Gly Asn Arg Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn
260 265 270

Thr Glu Gly Gln Tyr Cys Gln Arg Cys Lys Pro Gly Phe Tyr Arg Asp
275 280 285

Leu Arg Arg Pro Phe Ser Ala Pro Asp Ala Cys Lys Arg Lys
290 295 300

<210> 21
<211> 2010
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (243)..(1658)

<400> 21
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ctcccgccg ggcgcctcggc tttgtgcgag gagatggtgt agcccccctgg cgcgcgaaga 120
ggagccggac acttgtctcc cgtctccgag ctgctccca cccctggagg agagaccccc 180
ccctcggctc ggccgccttct gcgtctcccg gctggtgggg aagcctctgc gccgcggca 240
cc atg agt gaa cag agt atc tgt cag gca aga gct gct gtg atg gtt 287
Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ala Val Met Val
1 5 10 15

tat gat gat gcc aat aag aag tgg gtg cca gct ggt ggc tca act gga 335
Tyr Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly
20 25 30

ttc agc aga gtt cat atc tat cac cat aca ggc aac aac aca ttc aga 383
Phe Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg
35 40 45

gtg gtg ggc agg aag att cag gac cat cag gtc gtg ata aac tgt gcc 431
Val Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala
50 55 60

att cct aaa ggg ttg aag tac aat caa gct aca cag acc ttc cac cag 479
Ile Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln
65 70 75

tgg cga gat gct aga cag gtg tat ggt ctc aac ttt ggc agc aaa gag 527
Trp Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu
80 85 90 95

gat gcc aat gtc ttc gca agt gcc atg atg cat gcc tta gaa gtg tta 575
Asp Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu
100 105 110

aat tca cag gaa aca ggg cca aca ttg cct aga caa aac tca caa cta 623
Asn Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu
115 120 125

cct gct caa gtt caa aat ggc cca tcc caa gaa gaa ttg gaa att caa 671

Pro Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln		
130	135	140
aga aga caa cta caa gaa cag caa cgg caa aag gag ctg gag cgg gaa	719	
Arg Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu		
145	150	155
agg ctg aag cga gaa aga atg gaa aga gaa agg aag aag aga gag agg	767	
Arg Leu Lys Arg Glu Arg Met Glu Arg Glu Arg Lys Lys Arg Glu Arg		
160	165	170
175		
tta gaa agg gaa agg ctg gag agg gag cga ctg gaa caa gaa cag ctg	815	
Leu Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu		
180	185	190
gag aga gag aga caa gaa cgg gaa cgg cag gaa cgc ctg gag cgg cag	863	
Glu Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln		
195	200	205
gaa cgc ctg gag cgg cag gaa cgc ctg gag cgg cag gaa cgc ctg gat	911	
Glu Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp		
210	215	220
cg ^g gag agg caa gaa aga caa gaa cga gag agg ctg gag aga ctg gaa	959	
Arg Glu Arg Gln Glu Arg Gln Glu Arg Glu Arg Leu Glu Arg Leu Glu		
225	230	235
cg ^g gag agg caa gaa agg gag cga caa gag cag tta gaa agg gaa cag	1007	
Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Gln Leu Glu Arg Glu Gln		
240	245	250
255		
ctg gaa tgg gag aga gag cgc aga ata tca agt gct gct gcc cct gcc	1055	
Leu Glu Trp Glu Arg Glu Arg Arg Ile Ser Ser Ala Ala Ala Pro Ala		
260	265	270
tct gtt gag act cct cta aac tct gtg ctg gga gac tct tct gct tct	1103	
Ser Val Glu Thr Pro Leu Asn Ser Val Leu Gly Asp Ser Ser Ala Ser		
275	280	285
gag cca ggc ttg cag gca gcc tct cag ccg gcc gag act cca tcc caa	1151	
Glu Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Thr Pro Ser Gln		
290	295	300
300		
cag gaa gac aat cgc cct tta act gga ctt gca gct gca att gcc gga	1199	
Gln Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala Gly		
305	310	315
315		
gca aaa ctt agg aaa gtg tca cgg atg gag gat acc tct ttc cca agt	1247	
Ala Lys Leu Arg Lys Val Ser Arg Met Glu Asp Thr Ser Phe Pro Ser		
320	325	330
335		
gga ggg aat gct att ggt gtg aac tcc gcc tca tct aaa aca gat aca	1295	
Gly Gly Asn Ala Ile Gly Val Asn Ser Ala Ser Ser Lys Thr Asp Thr		
340	345	350
350		
ggc cgt gga aat gga ccc ctt cct tta ggg ggt agt ggt tta atg gaa	1343	
Gly Arg Gly Asn Gly Pro Leu Pro Leu Gly Gly Ser Gly Leu Met Glu		

355

360

365

gaa atg agt gcc ctg ctg gcc acg agg aga aga att gct gaa aag gga 1391
 Glu Met Ser Ala Leu Leu Ala Thr Arg Arg Arg Ile Ala Glu Lys Gly
 370 375 380

tca aca ata gaa aca gaa caa aaa gag gac aaa ggt gaa gat tca gag 1439
 Ser Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu
 385 390 395

cct gta act tct aag gcc tct tca aca agt aca cct gaa cca aca aga 1487
 Pro Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg
 400 405 410 415

aaa cct tgg gaa aga aca aat aca atg aat ggc agc aag tca cct gtt 1535
 Lys Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val
 420 425 430

atc tcc aga cct cca agg aaa aat cag att gtt ttt gac aac agg tcc 1583
 Ile Ser Arg Pro Pro Arg Lys Asn Gln Ile Val Phe Asp Asn Arg Ser
 435 440 445

tat gat tca tta cac aga cca aaa tcc aca ccc gtt atc aca gcc cag 1631
 Tyr Asp Ser Leu His Arg Pro Lys Ser Thr Pro Val Ile Thr Ala Gln
 450 455 460

tgc caa tgg agt cca gac gga agg act tgactatgac aggctgaagc 1678
 Cys Gln Trp Ser Pro Asp Gly Arg Thr
 465 470

aggacatttt agatgaaatg agaaaagaat taacaaagct aaaagaagag ctcattgatg 1738

caatcaggca ggaactgagc aagtcaaata ctgcatacag gaacagacta aggagagata 1798

ggacttaat ctggaggaaa aatatcctac aaacaacaac tgttcacaac agcaaacc 1858

tacatttatg agctgtaaga agaaaatgga gacaaacaga aggaggaaa aaccaaccta 1918

ctctgaaagc cttagacat tatgactctg gtgataagct cttccctct ccgttgctg 1978

ctttttctg gccaacatca gaatggtaac ac 2010

<210> 22

<211> 472

<212> PRT

<213> Homo sapiens

<400> 22

Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ala Val Met Val Tyr
 1 5 10 15

Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly Phe
 20 25 30

Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg Val
 35 40 45

Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala Ile
50 55 60

Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln Trp
65 70 75 80

Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu Asp
85 90 95

Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu Asn
100 105 110

Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu Pro
115 120 125

Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln Arg
130 135 140

Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu Arg
145 150 155 160

Leu Lys Arg Glu Arg Met Glu Arg Glu Arg Lys Lys Arg Glu Arg Leu
165 170 175

Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu
180 185 190

Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu
195 200 205

Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp Arg
210 215 220

Glu Arg Gln Glu Arg Gln Glu Arg Glu Arg Leu Glu Arg Leu Glu Arg
225 230 235 240

Glu Arg Gln Glu Arg Glu Arg Gln Glu Gln Leu Glu Arg Glu Gln Leu
245 250 255

Glu Trp Glu Arg Glu Arg Arg Ile Ser Ser Ala Ala Ala Pro Ala Ser
260 265 270

Val Glu Thr Pro Leu Asn Ser Val Leu Gly Asp Ser Ser Ala Ser Glu
275 280 285

Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Thr Pro Ser Gln Gln
290 295 300

Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala Gly Ala
305 310 315 320

Lys Leu Arg Lys Val Ser Arg Met Glu Asp Thr Ser Phe Pro Ser Gly
325 330 335

Gly Asn Ala Ile Gly Val Asn Ser Ala Ser Ser Lys Thr Asp Thr Gly
340 345 350

Arg Gly Asn Gly Pro Leu Pro Leu Gly Gly Ser Gly Leu Met Glu Glu
 355 360 365
 Met Ser Ala Leu Leu Ala Thr Arg Arg Arg Ile Ala Glu Lys Gly Ser
 370 375 380
 Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu Pro
 385 390 395 400
 Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg Lys
 405 410 415
 Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val Ile
 420 425 430
 Ser Arg Pro Pro Arg Lys Asn Gln Ile Val Phe Asp Asn Arg Ser Tyr
 435 440 445
 Asp Ser Leu His Arg Pro Lys Ser Thr Pro Val Ile Thr Ala Gln Cys
 450 455 460
 Gln Trp Ser Pro Asp Gly Arg Thr
 465 470

<210> 23
 <211> 1952
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (243)..(1715)

<400> 23
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 ctcccgccg ggcgcctcgcc tttgtgcgag gagatggtgt agccccctgg cgcggaaaga 120
 ggagccggac acttgtctcc cgtctccgag ctgctccccca cccctggagg agagaccccc 180
 ccctcggctc ggccgccttc gcgtctcccg gctgggtgggg aagcctctgc gcccggca 240
 cc atg agt gaa cag agt atc tgt cag gca aga gct gct gtg atg gtt 287
 Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ala Val Met Val
 1 5 10 15
 tat gat gat gcc aat aag aag tgg gtg cca gct ggt ggc tca act gga 335
 Tyr Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly
 20 25 30
 ttc agc aga gtt cat atc tat cac cat aca ggc aac aac aca ttc aga 383
 Phe Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg
 35 40 45

gtg gtg ggc agg aag att cag gac cat cag gtc gtg ata aac tgt gcc	431
Val Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala	
50 55 60	
att cct aaa ggg ttg aag tac aat caa gct aca cag acc ttc cac cag	479
Ile Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln	
65 70 75	
tgg cga gat gct aga cag gtg tat ggt ctc aac ttt ggc agc aaa gag	527
Trp Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu	
80 85 90 95	
gat gcc aat gtc ttc gca agt gcc atg atg cat gcc tta gaa gtg tta	575
Asp Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu	
100 105 110	
aat tca cag gaa aca ggg cca aca ttg cct aga caa aac tca caa cta	623
Asn Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu	
115 120 125	
cct gct caa gtt caa aat ggc cca tcc caa gaa gaa ttg gaa att caa	671
Pro Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln	
130 135 140	
aga aga caa cta caa gaa cag caa cgg caa aag gag ctg gag cgg gaa	719
Arg Arg Gln Leu Gln Glu Gln Arg Gln Lys Glu Leu Glu Arg Glu	
145 150 155	
agg ctg aag cga gaa aga atg gaa aga gaa agg aag aag aga gag agg	767
Arg Leu Lys Arg Glu Arg Met Glu Arg Glu Arg Lys Lys Arg Glu Arg	
160 165 170 175	
tta gaa agg gaa agg ctg gag agg gag cga ctg gaa caa gaa cag ctg	815
Leu Glu Arg Glu Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu	
180 185 190	
gag aga gag aga caa gaa cgg gaa cgg cag gaa cgc ctg gag cgg cag	863
Glu Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln	
195 200 205	
gaa cgc ctg gag cgg cag gaa cgc ctg gag cgg cag gaa cgc ctg gat	911
Glu Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp	
210 215 220	
cgg gag agg caa gaa aga caa gaa cga gag agg ctg gag aga ctg gaa	959
Arg Glu Arg Gln Glu Arg Gln Glu Arg Glu Arg Leu Glu Arg Leu Glu	
225 230 235	
cgg gag agg caa gaa agg gag cga caa gag cag tta gaa agg gaa cag	1007
Arg Glu Arg Gln Glu Arg Gln Glu Gln Leu Glu Arg Glu Gln	
240 245 250 255	
ctg gaa tgg gag aga gag cgc aga ata tca agt gct gct gcc cct gcc	1055
Leu Glu Trp Glu Arg Glu Arg Arg Ile Ser Ser Ala Ala Ala Pro Ala	
260 265 270	
tct gtt gag act cct cta aac tct gtg ctg gga gac tct tct gct tct	1103

Ser Val Glu Thr Pro Leu Asn Ser Val	Leu Gly Asp Ser Ser Ala Ser		
275	280	285	
gag cca ggc ttg cag gca gcc tct cag ccg gcc gag act cca tcc caa			1151
Glu Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Thr Pro Ser Gln			
290	295	300	
cag gaa gac aat cgc cct tta act gga ctt gca gct gca att gcc gga			1199
Gln Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala Gly			
305	310	315	
gca aaa ctt agg aaa gtg tca cgg atg gag gat acc tct ttc cca agt			1247
Ala Lys Leu Arg Lys Val Ser Arg Met Glu Asp Thr Ser Phe Pro Ser			
320	325	330	335
gga ggg aat gct att ggt gtg aac tcc gcc tca tct aaa aca gat aca			1295
Gly Gly Asn Ala Ile Gly Val Asn Ser Ala Ser Ser Lys Thr Asp Thr			
340	345	350	
ggc cgt gga aat gga ccc ctt cct tta ggg ggt agt ggt tta atg gaa			1343
Gly Arg Gly Asn Gly Pro Leu Pro Leu Gly Ser Gly Leu Met Glu			
355	360	365	
gaa atg agt gcc ctg ctg gcc acg agg aga aga att gct gaa aag gga			1391
Glu Met Ser Ala Leu Leu Ala Thr Arg Arg Arg Ile Ala Glu Lys Gly			
370	375	380	
tca aca ata gaa aca gaa caa aaa gag gac aaa ggt gaa gat tca gag			1439
Ser Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu			
385	390	395	
cct gta act tct aag gcc tct tca aca agt aca cct gaa cca aca aga			1487
Pro Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg			
400	405	410	415
aaa cct tgg gaa aga aca aat aca atg aat ggc agc aag tca cct gtt			1535
Lys Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val			
420	425	430	
atc tcc aga cca aaa tcc aca ccc tta tca cag ccc agt gcc aat gga			1583
Ile Ser Arg Pro Lys Ser Thr Pro Leu Ser Gln Pro Ser Ala Asn Gly			
435	440	445	
gtc cag acg gaa gga ctt gac tat gac agg ctg aag cag gac att tta			1631
Val Gln Thr Glu Gly Leu Asp Tyr Asp Arg Leu Lys Gln Asp Ile Leu			
450	455	460	
gat gaa atg aga aaa gaa tta aca aag cta aaa gaa gag ctc att gat			1679
Asp Glu Met Arg Lys Glu Leu Thr Lys Leu Lys Glu Glu Leu Ile Asp			
465	470	475	
gca atc agg cag gaa ctg acg aag tca aat act gca tagaggaaca			1725
Ala Ile Arg Gln Glu Leu Ser Lys Ser Asn Thr Ala			
480	485	490	
gactaaggag agataggact ttaatctgga ggaaaaatat cctacaaaca acaactgttc			1785

acaacagcaa acccctacat ttatgagctg taagaagaaa atggagacaa acagaaggag 1845
ggaaaaacca acctactctg aaagccttca gacattatga ctctgggtat aagctttc 1905
cctctccgtt tgctgctttt ttctggccaa catcagaatg gtaacac 1952

<210> 24
<211> 491
<212> PRT
<213> Homo sapiens

<400> 24
Met Ser Glu Gln Ser Ile Cys Gln Ala Arg Ala Ala Val Met Val Tyr
1 5 10 15
Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly Phe
20 25 30
Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg Val
35 40 45
Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala Ile
50 55 60
Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln Trp
65 70 75 80
Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu Asp
85 90 95
Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu Asn
100 105 110
Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu Pro
115 120 125
Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln Arg
130 135 140
Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu Arg
145 150 155 160
Leu Lys Arg Glu Arg Met Glu Arg Glu Arg Lys Lys Arg Glu Arg Leu
165 170 175
Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu
180 185 190
Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu
195 200 205
Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp Arg
210 215 220
Glu Arg Gln Glu Arg Gln Glu Arg Glu Arg Leu Glu Arg Leu Glu Arg
225 230 235 240

Glu Arg Gln Glu Arg Glu Arg Gln Glu Gln Leu Glu Arg Glu Gln Leu
245 250 255

Glu Trp Glu Arg Glu Arg Arg Ile Ser Ser Ala Ala Ala Pro Ala Ser
260 265 270

Val Glu Thr Pro Leu Asn Ser Val Leu Gly Asp Ser Ser Ala Ser Glu
275 280 285

Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Thr Pro Ser Gln Gln
290 295 300

Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala Gly Ala
305 310 315 320

Lys Leu Arg Lys Val Ser Arg Met Glu Asp Thr Ser Phe Pro Ser Gly
325 330 335

Gly Asn Ala Ile Gly Val Asn Ser Ala Ser Ser Lys Thr Asp Thr Gly
340 345 350

Arg Gly Asn Gly Pro Leu Pro Leu Gly Gly Ser Gly Leu Met Glu Glu
355 360 365

Met Ser Ala Leu Leu Ala Thr Arg Arg Arg Ile Ala Glu Lys Gly Ser
370 375 380

Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu Pro
385 390 395 400

Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg Lys
405 410 415

Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val Ile
420 425 430

Ser Arg Pro Lys Ser Thr Pro Leu Ser Gln Pro Ser Ala Asn Gly Val
435 440 445

Gln Thr Glu Gly Leu Asp Tyr Asp Arg Leu Lys Gln Asp Ile Leu Asp
450 455 460

Glu Met Arg Lys Glu Leu Thr Lys Leu Lys Glu Glu Leu Ile Asp Ala
465 470 475 480

Ile Arg Gln Glu Leu Ser Lys Ser Asn Thr Ala
485 490

<210> 25
<211> 827
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (233)..(601)

<400> 25
gaattcgagc gcaggagctc cgttctcca cctgctcccg gggagctagt gggatccaga 60
gaatcacccg ctgatggttt ttgccccaggc ctgaaacaac cagagagcta cgggaaagga 120
aggcgttggc ttgccagagg aattttccaa gtgctcaaac gccaggctta cggcgcctgt 180
gatccgtcca ggaggacaaa gtgggatttg aggatccact ccacttctgc tc atg gcg 238
Met Ala
1
cgc cag ggc ctg ccc ctg cac gtg gcc aca ctg ctg act ggg ctg ctg 286
Arg Gln Gly Leu Pro Leu His Val Ala Thr Leu Leu Thr Gly Leu Leu
5 10 15
gaa tgc ctg ggc ttt gct ggc gtc ctc ttt ggc tgg cct tca cta gtg 334
Glu Cys Leu Gly Phe Ala Gly Val Leu Phe Gly Trp Pro Ser Leu Val
20 25 30
ttt gtc ttc aag aat gaa gat tac ttt aag gat ctg tgt gga cca gat 382
Phe Val Phe Lys Asn Glu Asp Tyr Phe Lys Asp Leu Cys Gly Pro Asp
35 40 45 50
gct ggg ccg att ggc aat gcc aca ggg cag gct gac tgc aaa gcc cag 430
Ala Gly Pro Ile Gly Asn Ala Thr Gly Gln Ala Asp Cys Lys Ala Gln
55 60 65
gat gag agg ttc tca ctc atc ttc acc ctg ggg tcc ttc atg aac aac 478
Asp Glu Arg Phe Ser Leu Ile Phe Thr Leu Gly Ser Phe Met Asn Asn
70 75 80
ttc atg aca ttc ccc act ggc tac atc ttt gac cgg ttc aag acc acc 526
Phe Met Thr Phe Pro Thr Gly Tyr Ile Phe Asp Arg Phe Lys Thr Thr
85 90 95
gtg gca cgc ctc ata gcc ata ttt ttc tac acc acc gcc aca ctc atc 574
Val Ala Arg Leu Ile Ala Ile Phe Phe Tyr Thr Thr Ala Thr Leu Ile
100 105 110
ata gcc ttc acc tct gca gct tct tta tgaaaaaggc atcagcctca 621
Ile Ala Phe Thr Ser Ala Ala Ser Leu
115 120
ggccctcctt catttcatac tctgtctgca agtacaccttgc atgttagcact cactttcctc 681
ctgatgcccc gggggcacat cccataccca ctgcccccca actacagcta tggcctgtgc 741
cctggaaatg gcaccacaaa ggaagagaag gaaacagctg agcatgaaaa cagggagcta 801
cagtcaaagg agttccttgc agcgaa 827

<210> 26
<211> 123

<212> PRT
<213> Homo sapiens

<400> 26
Met Ala Arg Gln Gly Leu Pro Leu His Val Ala Thr Leu Leu Thr Gly
1 5 10 15

Leu Leu Glu Cys Leu Gly Phe Ala Gly Val Leu Phe Gly Trp Pro Ser
20 25 30

Leu Val Phe Val Phe Lys Asn Glu Asp Tyr Phe Lys Asp Leu Cys Gly
35 40 45

Pro Asp Ala Gly Pro Ile Gly Asn Ala Thr Gly Gln Ala Asp Cys Lys
50 55 60

Ala Gln Asp Glu Arg Phe Ser Leu Ile Phe Thr Leu Gly Ser Phe Met
65 70 75 80

Asn Asn Phe Met Thr Phe Pro Thr Gly Tyr Ile Phe Asp Arg Phe Lys
85 90 95

Thr Thr Val Ala Arg Leu Ile Ala Ile Phe Phe Tyr Thr Thr Ala Thr
100 105 110

Leu Ile Ile Ala Phe Thr Ser Ala Ala Ser Leu
115 120

<210> 27
<211> 1063
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (48)..(944)

<400> 27
ctttttcag ataacatctt ctgagtcata accagcctgg gtccccc atg atc gtg 56
Met Ile Val
1

ggg tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg 104
Gly Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu
5 10 15

cag ctg gtg tct acc tgc gtg gcc ttc tcg ctg gtg gct agc gtg ggc 152
Gln Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly
20 25 30 35

gcc tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc ttc 200
Ala Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe
40 45 50

tgc ttc tcc gtc acc ctg atc atc ctc atc gtg gag ctg tgc ggg ctc 248

Cys	Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu	
																55
																60
																65
cag	gcc	cgc	ttc	ccc	ctg	tct	tgg	cgc	aac	ttc	ccc	atc	acc	ttc	gcc	296
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	Ala	
																70
																75
																80
tgc	tat	gct	gcc	ctc	ttc	tgc	ctc	tcg	gcc	tcc	atc	atc	tac	ccc	acc	344
Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr	Pro	Thr	
																85
																90
																95
acc	tat	gtc	cag	ttc	ctg	tcc	cac	ggc	cgt	tcg	cg	gac	cac	gcc	atc	392
Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp	His	Ala	Ile	
																100
																105
																110
																115
gcc	gcc	acc	ttc	ttc	tcc	tgc	atc	gct	tgt	gtg	gct	tac	gcc	acc	gaa	440
Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala	Tyr	Ala	Thr	Glu	
																120
																125
																130
gtg	gcc	tgg	acc	cg	gg	cc	gg	gag	atc	act	gg	tat	atg	gcc	488	
Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile	Thr	Gly	Tyr	Met	Ala	
																135
																140
																145
acc	gta	ccc	ggg	ctg	ctg	aag	gtg	ctg	gag	acc	ttc	gtt	gcc	tgc	atc	536
Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu	Thr	Phe	Val	Ala	Cys	Ile	
																150
																155
																160
atc	ttc	gct	ttc	atc	agc	gac	ccc	aac	ctg	tac	cag	cac	cag	ccg	gcc	584
Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn	Leu	Tyr	Gln	His	Gln	Pro	Ala	
																165
																170
																175
ctg	gag	tgg	tgc	gtg	gct	ttc	atc	tgc	ttc	atc	ctt	gtc	acc	gg	cc	632
Leu	Glu	Trp	Cys	Val	Ala	Val	Tyr	Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	
																180
																185
																190
																195
atc	gcc	atc	ctg	ctg	aac	ctg	ggg	gag	tgc	acc	aac	gtg	cta	ccc	atc	680
Ile	Ala	Ile	Leu	Leu	Asn	Leu	Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	
																200
																205
																210
ccc	tcc	ccc	agc	ttc	ctg	tcg	ggg	ctg	gcc	ttt	ctg	tct	gtc	ctc	cc	728
Pro	Phe	Pro	Ser	Phe	Leu	Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	
																215
																220
																225
tat	gcc	acc	gcc	ctt	ctc	tgg	ccc	ctc	tac	cag	ttc	gat	gag	aag	cc	776
Tyr	Ala	Thr	Ala	Leu	Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	
																230
																235
																240
tat	ggc	ggc	cag	cct	cg	cg	tcg	aga	gat	gta	agc	tgc	agc	ccg	cc	824
Tyr	Gly	Gly	Gln	Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	
																245
																250
																255
cat	gcc	tac	tac	gtg	tgt	gcc	tgg	gac	cg	cg	ctg	gct	gtg	gcc	atc	872
His	Ala	Tyr	Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	
																260
																265
																270
																275
ctg	acg	gcc	atc	aac	cta	ctg	gct	tat	gtg	gct	gac	ctg	gtg	cac	tct	920
Leu	Thr	Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	

280

285

290

gcc cac ctg gtt ttt gtc aag gtc taagactctc ccaagaggct cccgttccct 974
Ala His Leu Val Phe Val Lys Val
295

ctccaacctc tttgttcttc ttgcccgagt tttctttatg gagtacttct ttccctccgcc 1034
tttcctctgt tttcctcttc ctgtctcccc 1063

<210> 28
<211> 299
<212> PRT
<213> *Homo sapiens*

<400> 28
Met Ile Val Gly Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu
1 5 10 15

Arg Leu Leu Gln Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala
20 25 30

Ser Val Gly Ala Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr
35 40 45

Trp Cys Phe Cys Phe Ser Val Thr Leu Ile Ile Ile Leu Ile Val Glu Leu
50 55 60

Cys Gly Leu Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile
65 70 75 80

Thr Phe Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile
85 90 95

Tyr Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
100 105 110

His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr
115 120 125

Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly
130 135 140

Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val
145 150 155 160

Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His
165 170 175

Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile
180 185 190

Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val
195 200 205 .

Leu Pro Ile Pro Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser

210

215

220

Val Leu Leu Tyr Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe
 225 230 235 240

Asp Glu Lys Tyr Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys
 245 250 255

Ser Arg Ser His Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala
 260 265 270

Val Ala Ile Leu Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu
 275 280 285

Val His Ser Ala His Leu Val Phe Val Lys Val
 290 295

<210> 29

<211> 1890

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1890)

<400> 29

gga tcc ggt ttc cca gaa gat tct gag cca atc agt att tcg cat ggc 48
 Gly Ser Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
 1 5 10 15

aac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg 96
 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
 20 25 30

aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg 144
 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 35 40 45

aac gga acc ctc tac att gct gct agg gac cat att tat act gtt gat 192
 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 50 55 60

ata gac aca tca cac acg gaa gaa att tat tgt agc aaa aaa ctg aca 240
 Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
 65 70 75 80

tgg aaa tct aga cag gcc gat gta gac aca tgc aga atg aag gga aaa 288
 Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
 85 90 95

cat aag gat gag tgc cac aac ttt att aaa gtt ctt cta aag aaa aac 336
 His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
 100 105 110

gat gat gca ttg ttt gtc tgt gga act aat gcc ttc aac cct tcc tgc	384
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys	
115 120 125	
aga aac tat aag atg gat aca ttg gaa cca ttc ggg gat gaa ttc agc	432
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser	
130 135 140	
gga atg gcc aga tgc cca tat gat gcc aaa cat gcc aac gtt gca ctg	480
Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu	
145 150 155 160	
ttt gca gat gga aaa cta tac tca gcc aca gtg act gac ttc ctt gcc	528
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala	
165 170 175	
att gac gca gtc att tac cgg agt ctt gga gaa agc cct acc ctg cgg	576
Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg	
180 185 190	
acc gtc aag cac gat tca aaa tgg ttg aaa gaa cca tac ttt gtt caa	624
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln	
195 200 205	
gcc gtg gat tac gga gat tat atc tac ttc ttc agg gaa ata gca	672
Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Arg Glu Ile Ala	
210 215 220	
gtg gag tat aac acc atg gga aag gta gtt ttc cca aga gtg gct cag	720
Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln	
225 230 235 240	
gtt tgt aag aat gat atg gga gga tct caa aga gtc ctg gag aaa cag	768
Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln	
245 250 255	
tgg acg tcg ttc ctg aag gcg cgc ttg aac tgc tca gtt cct gga gac	816
Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp	
260 265 270	
tct cat ttt tat ttc aac att ctc cag gca gtt aca gat gtg att cgt	864
Ser His Phe Tyr Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg	
275 280 285	
atc aac ggg cgt gat gtt gtc ctg gca acg ttt tct aca cct tat aac	912
Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn	
290 295 300	
agc atc cct ggg tct gca gtc tgt gcc tat gac atg ctt gac att gcc	960
Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala	
305 310 315 320	
agt gtt ttt act ggg aga ttc aag gaa cag aag tct cct gat tcc acc	1008
Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr	
325 330 335	
tgg aca cca gtt cct gat gaa cga gtt cct aag ccc agg cca ggt tgc	1056

Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys			
340	345	350	
tgt gct ggc tca tcc tcc tta gaa aga tat gca acc tcc aat gag ttc			1104
Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe			
355	360	365	
cct gat gat acc ctg aac ttc atc aag acg cac ccg ctc atg gat gag			1152
Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu			
370	375	380	
gca gtg ccc tcc atc ttc aac agg cca tgg ttc ctg aga aca atg gtc			1200
Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val			
385	390	395	400
aga tac cgc ctt acc aaa att gca gtg gac aca gct gct ggg cca tat			1248
Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr			
405	410	415	
cag aat cac act gtg gtt ttt ctg gga tca gag aag gga atc atc ttg			1296
Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu			
420	425	430	
aag ttt ttg gcc aga ata gga aat agt ggt ttt cta aat gac agc ctt			1344
Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu			
435	440	445	
ttc ctg gag gag atg agt gtt tac aac tct gaa aaa tgc agc tat gat			1392
Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp			
450	455	460	
gga gtc gaa gac aaa agg atc atg ggc atg cag ctg gac aga gca agc			1440
Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser			
465	470	475	480
agc tct ctg tat gtt gcg ttc tct acc tgt gtg ata aag gtt ccc ctt			1488
Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu			
485	490	495	
ggc cgg tgt gaa cga cat ggg aag tgt aaa aaa acc tgt att gcc tcc			1536
Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser			
500	505	510	
aga gac cca tat tgt gga tgg ata aag gaa ggt ggt gcc tgc agc cat			1584
Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Ala Cys Ser His			
515	520	525	
tta tca ccc aac agc aga ctg act ttt gag cag gac ata gag cgt ggc			1632
Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly			
530	535	540	
aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat			1680
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn			
545	550	555	560
ggg cat tcc agt tcc ctc ttg ccc agc aca acc aca tca gat tcg acg			1728
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Ser Asp Ser Thr			

565

570

575

gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat 1776
 Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
 580 585 590

ctg ctt gac tca cct gac agc aca gac cct ttg ggg gca gtg tct tcc 1824
 Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
 595 600 605

cat aat cac caa gac aag gga gtg att cgg gaa agt tac ctc aaa 1872
 His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
 610 615 620

ggc cac gac cag ctc gag 1890
 Gly His Asp Gln Leu Glu
 625 630

<210> 30

<211> 630

<212> PRT

<213> Homo sapiens

<400> 30

Gly Ser Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
 1 5 10 15

Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
 20 25 30

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 35 40 45

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 50 55 60

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
 65 70 75 80

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
 85 90 95

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
 100 105 110

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
 115 120 125

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
 130 135 140

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
 145 150 155 160

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
 165 170 175

Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
180 185 190

Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
195 200 205

Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Arg Glu Ile Ala
210 215 220

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
225 230 235 240

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
245 250 255

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
260 265 270

Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
275 280 285

Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
290 295 300

Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
305 310 315 320

Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
325 330 335

Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
340 345 350

Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
355 360 365

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
370 375 380

Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
385 390 395 400

Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
405 410 415

Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
420 425 430

Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
435 440 445

Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
450 455 460

Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
465 470 475 480

Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
 485 490 495
 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
 500 505 510
 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
 515 520 525
 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
 530 535 540
 Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
 545 550 555 560
 Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
 565 570 575
 Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
 580 585 590
 Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
 595 600 605
 His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
 610 615 620
 Gly His Asp Gln Leu Glu
 625 630

<210> 31
 <211> 1356
 <212> DNA
 <213> Homo sapiens

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 cggccggggcc tctccgaggt cccgcagggt attccctcga acacccggta cctcaacctc 120
 atggagaaca acatccagat gatccaggcc gacacccctcc gccacacctca ccacctggag 180
 gtcctgcagt tgggcagggaa ctccatccgg cagattgagg tgggggcctt caacggcctg 240
 gccagcctca acacccttggaa gctgttcgac aactggctga cagtcatccc tagcggggcc 300
 tttgaatacc tggccaaatgt gcggggagctc tggcttcgca acaaccccat cgaaagcatc 360
 ccctcttacg tcttcaaccg ggtgccttcc ctcatgcgcc tggacttggg ggagctcaag 420
 aagctggagt atatctctga gggagctttt gaggggtgt tcaacactcaa gtatctgaac 480
 ttgggcattgt gcaacattaa agacatgccc aatctcaccc ccctgggtggg gctggaggag 540
 ctggagatgt cagggaaacca cttccctgag atcaggcctg gctccttcca tggcctgagc 600
 tccctcaaga agctctgggt catgaactca caggtcagcc tgattgagcg gaatgtttt 660
 gacgggctgg cttcaactgtt ggaactcaac ttggcccaaca ataacactctc ttctttgccc 720
 catgacctct ttacccctgtt gaggtacctg gtggaggatgc atctacacca caacccttgg 780
 aactgtgatt gtgacattct gtggcttagcc tgggtggcttc gagagtataat acccaccaat 840
 tccacactgtt gtggccgctg tcatgctccc atgcacatgc gaggccgcta cctcggtgg 900
 gtggaccagg cctccttcca gtgctctgcc cccttcatca tgacgcacc tcgagacctc 960
 aacatttctg agggtcggat ggcagaactt aagtgtcgga ctccccctat gtcctccgtg 1020
 aagtggttgc tgcccaatgg gacagtgtc agccatgcct cccgccaccc aaggatctct 1080

gtcctcaacg acggcacctt gaactttcc cacgtgctgc tttcagacac cgggggtgtac 1140
acatgcatgg tgaccaatgt tgcaaggcaac tccaaacgcct cggcctaccc caatgtgagc 1200
acggctgagc ttaacacccctc caactacagc ttcttcacca cagtaacagt ggagaccacg 1260
gagatctcgc ctgaggacac aacgcgaaag tacaagcctg ttcctaccac gtccactggt 1320
taccagccgg catataccac ctctaccacg gtcgag 1356

<210> 32
<211> 448
<212> PRT
<213> Homo sapiens

<400> 32
Asn Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val
1 5 10 15

Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser Asn
20 25 30

Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile Gln Met Ile Gln Ala
35 40 45

Asp Thr Phe Arg His Leu His Leu Glu Val Leu Gln Leu Gly Arg
50 55 60

Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe Asn Gly Leu Ala Ser
65 70 75 80

Leu Asn Thr Leu Glu Leu Phe Asp Asn Trp Leu Thr Val Ile Pro Ser
85 90 95

Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg Glu Leu Trp Leu Arg Asn
100 105 110

Asn Pro Ile Glu Ser Ile Pro Ser Tyr Ala Phe Asn Arg Val Pro Ser
115 120 125

Leu Met Arg Leu Asp Leu Gly Glu Leu Lys Lys Leu Glu Tyr Ile Ser
130 135 140

Glu Gly Ala Phe Glu Gly Leu Phe Asn Leu Lys Tyr Leu Asn Leu Gly
145 150 155 160

Met Cys Asn Ile Lys Asp Met Pro Asn Leu Thr Pro Leu Val Gly Leu
165 170 175

Glu Glu Leu Glu Met Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly
180 185 190

Ser Phe His Gly Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser
195 200 205

Gln Val Ser Leu Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu
210 215 220

Val Glu Leu Asn Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp
225 230 235 240

Leu	Phe	Thr	Pro	Leu	Arg	Tyr	Leu	Val	Glu	Leu	His	Leu	His	His	Asn
245									250					255	
Pro	Trp	Asn	Cys	Asp	Cys	Asp	Ile	Leu	Trp	Leu	Ala	Trp	Trp	Leu	Arg
260								265					270		
Glu	Tyr	Ile	Pro	Thr	Asn	Ser	Thr	Cys	Cys	Gly	Arg	Cys	His	Ala	Pro
275								280					285		
Met	His	Met	Arg	Gly	Arg	Tyr	Leu	Val	Glu	Val	Asp	Gln	Ala	Ser	Phe
290								295				300			
Gln	Cys	Ser	Ala	Pro	Phe	Ile	Met	Asp	Ala	Pro	Arg	Asp	Leu	Asn	Ile
305								310			315		320		
Ser	Glu	Gly	Arg	Met	Ala	Glu	Leu	Lys	Cys	Arg	Thr	Pro	Pro	Met	Ser
325								330			335				
Ser	Val	Lys	Trp	Leu	Leu	Pro	Asn	Gly	Thr	Val	Leu	Ser	His	Ala	Ser
340								345			350				
Arg	His	Pro	Arg	Ile	Ser	Val	Leu	Asn	Asp	Gly	Thr	Leu	Asn	Phe	Ser
355								360			365				
His	Val	Leu	Leu	Ser	Asp	Thr	Gly	Val	Tyr	Thr	Cys	Met	Val	Thr	Asn
370								375			380				
Val	Ala	Gly	Asn	Ser	Asn	Ala	Ser	Ala	Tyr	Leu	Asn	Val	Ser	Thr	Ala
385								390			395		400		
Glu	Leu	Asn	Thr	Ser	Asn	Tyr	Ser	Phe	Phe	Thr	Thr	Val	Thr	Val	Glu
405								410			415				
Thr	Thr	Glu	Ile	Ser	Pro	Glu	Asp	Thr	Thr	Arg	Lys	Tyr	Lys	Pro	Val
420								425			430				
Pro	Thr	Thr	Ser	Thr	Gly	Tyr	Gln	Pro	Ala	Tyr	Thr	Thr	Ser	Thr	Thr
435								440			445				

<210> 33

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

ggatccgggtt tccccagaaga ttcttgagccca atc 33

<210> 34

<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
ctcgagctgg tcgtggcctt tgaggtaact ttc 33

<210> 35
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
cacaagccag gacggaaca 19

<210> 36
<211> 19
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 36
tggaactaat gccttcaac 19

<210> 37
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
gagtcctgga gaaacagtgg a 21

<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
atgaggcagt gccctccatc 20

<210> 39
<211> 19
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 39
ccatattgtg gatggataa 19

<210> 40
<211> 19
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 40
gacactcaat ccaaagacc 19

<210> 41
<211> 19
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 41
ccatcacgca gcagggcta 19

<210> 42
<211> 30
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 42
ctcgtcctcg agggttaagcc tatccctaac 30

<210> 43
<211> 31
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<220>
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<400> 43
ctcgtcgggc ccctgatcag cgggtttaaa c 31

<210> 44
<211> 38
<212> DNA
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<220>
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<400> 44
ctcgtcggat ccaactgccc ctccgtctgc tcgtgcag 38

<210> 45
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<220>
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ctcgtcgtcg accgtggtag aggtggata tgccggctg 39

<210> 46
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 46
gtgcagtaac cagttcagca 20

<210> 47
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 47
acctgtccaa gctgcggag 20

<210> 48
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 48
ttgacgggct ggcttcaactt 20

<210> 49
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 49
gacagtgcctc agccacgcct 20

<210> 50
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
cctttcaaaa tcctctctga ctcac 25

<210> 51
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 51
tcaccgaaga aaaacgacac ac 22

<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 52
cctggcaccc tggcagctca ga 22

<210> 53

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 53
catcttcaac aggccatggt t 21

<210> 54
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 54
agcagctgtg tccactgcaa 20

<210> 55
<211> 31
<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 55
tgagaacaat ggtcagatac cgccttacca a 31

<210> 56
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 56
cgcagtcatt taccggagtc tt 22

<210> 57
<211> 24
<212> DNA
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<220>
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<400> 57
ttctttcaac cattttgaat cgtg 24

<210> 58
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<400> 58
agccctaccc tgcggaccgt ca 22

<210> 59
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<400> 59
tcctttgtgg cactgaatgg 20

<210> 60
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<400> 60
ccctcttgag ccgtcgaa 18

<210> 61
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<220>
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<400> 61
tccctcttgc ccagcacaac cac 23

<210> 62
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 62
cgcgaaagta caagcctgtt c 21

<210> 63
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 63
gaatgagcac cgtggtagag g 21

<210> 64
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 64
cgtccactgg ttaccagccg gcatata 27

<210> 65
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 65
tggactcatc ccacttgctc t 21

<210> 66
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 66
cctgcgcaaa aagttgtgaa 20

<210> 67
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 67
cagctgaatc ctgacatcat atccacactg tgt 33

<210> 68
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 68
tctctgtctg cagtacctgg cat 23

<210> 69
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 69
ggcagtgggt atgggatgtg 20

<210> 70
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 70
actttcctcc tcatgcggcg gg 22

<210> 71
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 71
aaaggcgag gaaagaagta ctc 23

<210> 72

<211> 18
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

<400> 72
 gctcccggttc cctctcca 18

<210> 73
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 73
 cctcttgg tttttttttt tttttttttt 31

<210> 74
 <211> 1287
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(978)

<220>
 <221> misc_feature
 <222> (1139)..(1172)
 <223> an n may be any one of a or t or g or c

<400> 74
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 Ala Ser Leu Thr Cys Ser Pro Leu Asp Pro Glu Val Gly Pro Tyr Cys
 1 5 10 15

gac aca cct acc atg cgg aca ctc ttc aac ctc ctc tgg ctt gcc ctg 96
 Asp Thr Pro Thr Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu
 20 25 30

gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc aaa aaa 144
 Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys
 35 40 45

gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat aag ccg 192
 Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro
 50 55 60

gtg caa gac cgg ggt ttg gtg acg gac ctc aaa gct gag agt gtg 240
 Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val
 65 70 75 80

gtt ctt gag cat cgc agc tac tgc tcg gca aag gcc cgg gac aga cac	288
Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His	
85 90 95	
ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc cat ggc	336
Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly	
100 105 110	
tac gat gtc acc aag gtc ttt ggg aag ttc aca cag atc tca ccc	384
Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro	
115 120 125	
gtc tgg ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag gtc acg	432
Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr	
130 135 140	
ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg aag cat	480
Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His	
145 150 155 160	
gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac tgg act	528
Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr	
165 170 175	
tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata gag gag	576
Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu	
180 185 190	
ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc gat ggc	624
Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly	
195 200 205	
ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc gtg ggc	672
Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly	
210 215 220	
ctc atc cac atg ctc acc cac ttg gcc gag gct ctg cac cag gcc cgg	720
Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg	
225 230 235 240	
ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg acc gac	768
Leu Leu Ala Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp	
245 250 255	
cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc ccc gtg	816
Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val	
260 265 270	
ctg gat ggt ttc agc ctc atg acc tac gac tac gca aca ctg tcc tgg	864
Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp	
275 280 285	
gtt cga gcc tgc gtc cag gtc gat ccc tgg ggc tca act tct atg	912
Val Arg Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met	
290 295 300	

gta tgg act acg cga cct cca agg atg ccc gtg agc ctg ttg tcg ggg	960																		
Val Trp Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly																			
305	310	315	320	cca ggt aca tcc aga cac tgaaggacca caggccccgg atggtgtggg	1008	Pro Gly Thr Ser Arg His		325		acggccaggc ctcagagcac ttcttcgagt acaagaagag ccgcagtggg aggcacgtcg	1068	tcttctaccc aaccctgaag tccctgcagg tgcggctgga gctggcccg gagctggcg	1128	ttggggtctc natntggag ctgggccagg gcctggacta cttntacgac ctgctctagg	1188	tggcattgc ggcctccgag gtggacgtgt tctttctaa gccatggagt gagtgagcag	1248	gtgtgaaata caggcctcca ctccgtttac aaaaaaaaaa	1287
315	320																		
cca ggt aca tcc aga cac tgaaggacca caggccccgg atggtgtggg	1008																		
Pro Gly Thr Ser Arg His																			
325																			
acggccaggc ctcagagcac ttcttcgagt acaagaagag ccgcagtggg aggcacgtcg	1068																		
tcttctaccc aaccctgaag tccctgcagg tgcggctgga gctggcccg gagctggcg	1128																		
ttggggtctc natntggag ctgggccagg gcctggacta cttntacgac ctgctctagg	1188																		
tggcattgc ggcctccgag gtggacgtgt tctttctaa gccatggagt gagtgagcag	1248																		
gtgtgaaata caggcctcca ctccgtttac aaaaaaaaaa	1287																		

<210> 75
 <211> 326
 <212> PRT
 <213> Homo sapiens

Asp Thr Pro Thr Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu			
1	5	10	15
20	25	30	
Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys			
35	40	45	
Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro			
50	55	60	
Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val			
65	70	75	80
Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His			
85	90	95	
Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly			
100	105	110	
Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro			
115	120	125	
Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr			
130	135	140	
Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His			
145	150	155	160
Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr			
165	170	175	

Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu
180 185 190

Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly
195 200 205

Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly
210 215 220

Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg
225 230 235 240

Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp
245 250 255

Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val
260 265 270

Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp
275 280 285

Val Arg Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met
290 295 300

Val Trp Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly
305 310 315 320

Pro Gly Thr Ser Arg His
325

<210> 76
<211> 1291
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (299)..(982)

<220>
<221> misc_feature
<222> (1143)..(1176)
<223> an n may be any one of a or t or g or c

<400> 76
gcctccctga catgcagccc tctggacccc gaggttggac cctactgtga cacacctacc 60
atgcggacac tcttcaacct cctctggctt gccctggcct gcagccctgt tcacactacc 120
ctgtcaaagt cagatgccaa aaaagccgcc tcaaagacgc tgctggagaa gagtcagttt 180
tcagataagc cggtgcaaga ccggggtttg gtggtgacgg acctcaaagc tgagagtgtg 240
gttcttgagc atcgcagcta ctgctcggca aaggccccggg acagacactt tgctgggg 298

atg tac tgg gct atg tca ctc cac cag tgg aac agc cat ggc tac gat	346
Met Tyr Trp Ala Met Ser Leu His Gln Trp Asn Ser His Gly Tyr Asp	
1 5 10 15	
gtc acc aag gtc ttt ggg agc aag ttc aca cag atc tca ccc gtc tgg	394
Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp	
20 25 30	
ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag gtc acg ggc ctc	442
Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu	
35 40 45	
cac gac gtg gac caa ggg tgg atg cga gct gtc agg aag cat gcc aag	490
His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys	
50 55 60	
ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac tgg act tac gat	538
Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp	
65 70 75 80	
gat ttc cgg aac gtc tta gac agt gag gat gag ata gag gag ctg agc	586
Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser	
85 90 95	
aag acc gtg gtc cag gtg gca aag aac cag cat ttc gat ggc ttc gtg	634
Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val	
100 105 110	
gtg gag gtc tgg aac cag ctg cta agc cag aag cgc gtg ggc ctc atc	682
Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile	
115 120 125	
cac atg ctc acc cac ttg gcc gag gct ctg cac cag gcc cgg ctg ctg	730
His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu	
130 135 140	
gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg acc gac cag ctg	778
Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu	
145 150 155 160	
ggc atg ttc acg cac aag gag ttt gag cag ctg gcc ccc gtc ctg gat	826
Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp	
165 170 175	
ggt ttc agc ctc atg acc tac gac tac gca aca ctg tcc tgg gtt cga	874
Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp Val Arg	
180 185 190	
gcc tgc gtc cag gtc ctg gat ccc tgg ggc tca act tct atg gta tgg	922
Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met Val Trp	
195 200 205	
act acg cga cct cca agg atg ccc gtg agc ctg ttg tcg ggg cca ggt	970
Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly Pro Gly	
210 215 220	

aca tcc aga cac tgaaggacca caggccccgg atggtgtggg acggccaggc 1022
Thr Ser Arg His
225

ctcagagcac ttcttcgagt acaagaagag ccgcagtggg aggcacgtcg tcttctaccc 1082
aaccctgaag tccctgcagg tgcggctgga gctggcccg gagctgggcg ttggggtctc 1142
natntggag ctgggccagg gcctggacta cttnaacgac ctgctctagg tgggcattgc 1202
ggcctccgcg gtggacgtgt tctttctaa gccatggagt gagtgagcag gtgtgaaata 1262
caggcctcca ctccgtttac aaaaaaaaaa 1291

<210> 77
<211> 228
<212> PRT
<213> Homo sapiens

<400> 77
Met Tyr Trp Ala Met Ser Leu His Gln Trp Asn Ser His Gly Tyr Asp
1 5 10 15

Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp
20 25 30

Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu
35 40 45

His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys
50 55 60

Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp
65 70 75 80

Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser
85 90 95

Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val
100 105 110

Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile
115 120 125

His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu
130 135 140

Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu
145 150 155 160

Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp
165 170 175

Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp Val Arg
180 185 190

Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met Val Trp
195 200 205

Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly Pro Gly
210 215 220

Thr Ser Arg His
225

<210> 78
<211> 816
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(628)

<400> 78

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Arg Val Leu Val Leu Met Val Gly Ala Val Met Phe Thr Arg Gly Ser
1 5 10 15

ccg gcc gcg tgg ggg cgc gcc agg gag aat atc tgc ttg ctc aac ttt 97
Pro Ala Ala Trp Gly Arg Ala Arg Glu Asn Ile Cys Leu Leu Asn Phe
20 25 30

ttc tgt ggc acc atc gtg ctc atc ttc ttc ctg gag ctg gct gtg gcc 145
Phe Cys Gly Thr Ile Val Leu Ile Phe Leu Glu Leu Ala Val Ala
35 40 45

gtg ctg gcc ttc ctg ttc cag gac tgg gtg agg gac cgg ttc cgg gag 193
Val Leu Ala Phe Leu Phe Gln Asp Trp Val Arg Asp Arg Phe Arg Glu
50 55 60

ttc ttc gag agc aac atc aag tcc tac cgg gac gat atc gat ctg caa 241
Phe Phe Glu Ser Asn Ile Lys Ser Tyr Arg Asp Asp Ile Asp Leu Gln
65 70 75 80

aac ctc atc gac tcc ctt cag aaa gct aac cag tgc tgt ggc gca tat 289
Asn Leu Ile Asp Ser Leu Gln Lys Ala Asn Gln Cys Cys Gly Ala Tyr
85 90 95

ggc cct gaa gac tgg gac ctc aac gtc tac ttc aat tgc agc ggt gcc 337
Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr Phe Asn Cys Ser Gly Ala
100 105 110

agc tac agc cga gag aag tgc ggg gtc ccc ttc tcc tgc tgc gtg cca 385
Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser Cys Cys Val Pro
115 120 125

gat cct gcg caa aaa gtt gtg aac aca cag tgt gga tat gat gtc agg 433
Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly Tyr Asp Val Arg
130 135 140

att cag ctg aag agc aag tgg gat gag tcc atc ttc acg aaa ggc tgc 481
Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser Ile Phe Thr Lys Gly Cys
145 150 155 160

atc cag gcg ctg gaa agc tgg ctc ccg cgg aac att tac att gtg gct 529
Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile Tyr Ile Val Ala
165 170 175

ggc gtc ttc atc gcc atc tcg ctg ttg cag ata ttt ggc atc ttc ctg 577
Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe Gly Ile Phe Leu
180 185 190

gca agg acg ctg atc tca gac atc gag gca gtg aag gcc ggc cat cac 625
Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys Ala Gly His His
195 200 205

ttc tgaggagcag agttgaggga gccgagctga gccacgctgg gaggccagag 678
Phe

cctttctctg ccatcagccc tacgtccaga gggagaggag ccgacacccc cagagccagt 738
gccccatctt aagcatcagc gtgacgtgac ctctctgttt ctgcttgctg gtgctgaaga 798
ccaagggtcc cccttgtt 816

<210> 79
<211> 209
<212> PRT
<213> Homo sapiens

<400> 79
Arg Val Leu Val Leu Met Val Gly Ala Val Met Phe Thr Arg Gly Ser
1 5 10 15

Pro Ala Ala Trp Gly Arg Ala Arg Glu Asn Ile Cys Leu Leu Asn Phe
20 25 30

Phe Cys Gly Thr Ile Val Leu Ile Phe Phe Leu Glu Leu Ala Val Ala
35 40 45

Val Leu Ala Phe Leu Phe Gln Asp Trp Val Arg Asp Arg Phe Arg Glu
50 55 60

Phe Phe Glu Ser Asn Ile Lys Ser Tyr Arg Asp Asp Ile Asp Leu Gln
65 70 75 80

Asn Leu Ile Asp Ser Leu Gln Lys Ala Asn Gln Cys Cys Gly Ala Tyr
85 90 95

Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr Phe Asn Cys Ser Gly Ala
100 105 110

Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser Cys Cys Val Pro
115 120 125

Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly Tyr Asp Val Arg

130	135	140
Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser Ile Phe Thr Lys Gly Cys		
145 . 150	155	160
Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile Tyr Ile Val Ala		
165	170	175
Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe Gly Ile Phe Leu		
180	185	190
Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys Ala Gly His His		
195	200	205

Phe

<210> 80
<211> 2574
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (63)..(1022)

<400> 80
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cc atg tcc aac ccc agc gcc cca cca tat gaa gac cgc aac ccc	107
Met Ser Asn Pro Ser Ala Pro Pro Pro Tyr Glu Asp Arg Asn Pro	
1 5 10 15	

ctg tac cca ggc cct ctg ccc cct ggg ggc tat ggg cag cca tct gtc	155
Leu Tyr Pro Gly Pro Leu Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val	
20 25 30	

ctg cca gga ggg tat cct gcc tac cct ggc tac ccg cag cct ggc tac	203
Leu Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr	
35 40 45	

ggt cac cct gct ggc tac cca cag ccc atg ccc ccc acc cac ccg atg	251
Gly His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met	
50 55 60	

ccc atg aac tac ggc cca ggc cat ggc tat gat ggg gag gag aga gcg	299
Pro Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala	
65 70 75	

gtg agt gat agc ttc ggg cct gga gag tgg gat gac cgg aaa gtg cga	347
Val Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg	
80 85 90 95	

cac act ttt atc cga aag gtt tac tcc atc atc tcc gtg cag ctg ctc	395
His Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu	

100	105	110	
atc act gtg gcc atc att gct atc ttc acc ttt gtg gaa cct gtc agc Ile Thr Val Ala Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser 115	120	125	443
gcc ttt gtg agg aga aat gtg gct gtc tac tac gtg tcc tat gct gtc Ala Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val 130	135	140	491
ttc gtt gtc acc tac ctg atc ctt gcc tgc tgc cag gga ccc aga cgc Phe Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg 145	150	155	539
cgt ttc cca tgg aac atc att ctg ctg acc ctt ttt act ttt gcc atg Arg Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met 160	165	170	587
ggc ttc atg acg ggc acc att tcc agt atg tac caa acc aaa gcc gtc Gly Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val 180	185	190	635
atc att gca atg atc atc act gcg gtg gta tcc att tca gtc acc atc Ile Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile 195	200	205	683
ttc tgc ttt cag acc aag gtg agg gca tgg agg gcc ctt ccc tgg ccc Phe Cys Phe Gln Thr Lys Val Arg Ala Trp Arg Ala Leu Pro Trp Pro 210	215	220	731
ccc gac tcc cct ttc tta tca ggc ccg gac ccc ggt aca cta ggg atg Pro Asp Ser Pro Phe Leu Ser Gly Pro Asp Pro Gly Thr Leu Gly Met 225	230	235	779
ttc cct aga gac ctg atc ccc ttc tcc tca tcc gca cct aca aaa ctg Phe Pro Arg Asp Leu Ile Pro Phe Ser Ser Ala Pro Thr Lys Leu 240	245	250	827
tgt cct gtt tct gtc ctt aga atg ttg tgg aca ttc cca tac ccc cta Cys Pro Val Ser Val Leu Arg Met Leu Trp Thr Phe Pro Tyr Pro Leu 260	265	270	875
gga ggc agc act ggg act ccc tgg cag ggc cag tct gac tgg gct ggt Gly Gly Ser Thr Gly Thr Pro Trp Gln Gly Gln Ser Asp Trp Ala Gly 275	280	285	923
tgt cac agc cat ctg aca ggt gcc tct ttc ttg ctt cct ggc agg tgg Cys His Ser His Leu Thr Gly Ala Ser Phe Leu Leu Pro Gly Arg Trp 290	295	300	971
act tca cct cgt gca cag gcc tct tct gtg tcc tgg gaa ttg tgc tcc Thr Ser Pro Arg Ala Gln Ala Ser Ser Val Ser Trp Glu Leu Cys Ser 305	310	315	1019
tgg tgactggat tgtcaactagc atttgtctct tagcattgtg ctctacttcc Trp 320			1072

aatacgttta ctggctccac atgctctatg ctgctctggg ggccatttgt ttcaccctgt 1132
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acaggcttct tgactacgta gttggagcta tttcttcccc cagcaaagcc agagagctt 1732
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aaagtaacct atacaggcca gcatggaaca gcatctcccc tgggcttgct cctggcttgt 1972
gacgctataa gacagagcag gccacatgtg gccattctgc tccccatttc tgaaagctgc 2032
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gtgaagagag actcggtgcg ggcagggaga atgcctgggg gtccctcacc tggcttaggga 2212
gataccgaag cctactgtgg tactgaagac ttctgggttc tttccttctg ctaaccagg 2272
gagggtccta agaggaaggt gacttctctc tgtttgcatt aagttgcact gggggatttc 2332
tgacttgagg cccatctctc cagccagcca ctgccttctt tgtaatatta agtgccttga 2392
gctggaatgg ggaagggggca caagggtcag tctgtcgggt gggggcagaa atcaaatcag 2452
cccaaggata tagttaggat taattactta atagagaaa cctaactata tcacacaaag 2512
ggatacaact ataaatgtaa taaaatttat gtctagaagt taaaaaaaaaaa aaaaaaaaaa 2572
gt 2574

<210> 81
<211> 320
<212> PRT

<213> Homo sapiens

<400> 81

Met Ser Asn Pro Ser Ala Pro Pro Pro Tyr Glu Asp Arg Asn Pro Leu
1 5 10 15

Tyr Pro Gly Pro Leu Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu
20 25 30

Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr Gly
35 40 45

His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro
50 55 60

Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val
65 70 75 80

Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His
85 90 95

Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu Ile
100 105 110

Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser Ala
115 120 125

Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe
130 135 140

Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg
145 150 155 160

Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly
165 170 175

Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile
180 185 190

Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe
195 200 205

Cys Phe Gln Thr Lys Val Arg Ala Trp Arg Ala Leu Pro Trp Pro Pro
210 215 220

Asp Ser Pro Phe Leu Ser Gly Pro Asp Pro Gly Thr Leu Gly Met Phe
225 230 235 240

Pro Arg Asp Leu Ile Pro Phe Ser Ser Ser Ala Pro Thr Lys Leu Cys
245 250 255

Pro Val Ser Val Leu Arg Met Leu Trp Thr Phe Pro Tyr Pro Leu Gly
260 265 270

Gly Ser Thr Gly Thr Pro Trp Gln Gly Gln Ser Asp Trp Ala Gly Cys
275 280 285

His Ser His Leu Thr Gly Ala Ser Phe Leu Leu Pro Gly Arg Trp Thr
290 295 300

Ser Pro Arg Ala Gln Ala Ser Ser Val Ser Trp Glu Leu Cys Ser Trp
305 310 315 320